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Run on:

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Sequence 20, 13 Sequence 1, M Sequence 1, Sequence 1, Sequence 1, M Sequence 1, M Sequence 1, M Sequence 42, 2 Sequence 42, 2
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                                 Sequence
                                                                   Sequence
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Wilcholas F.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HARONED HUMANIZED IMMUNOGLOBLINS
CONFESSOURNES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRELING STATEM:
CURRELING STATEM:
CURRELING APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION DATA:
FILING DATE:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CILING DATE:
APPLICATION DATA:
FILING DATE:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
TILING DATE:
TEMPORATE TO STATEMENT OF THE STATEMENT 
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          US-08-474-040-83
US-08-444-200-83
US-08-444-200-83
US-08-436-463-4
US-08-436-463-4
US-08-436-463-4
US-08-1042-20
US-08-1042-245-4
US-08-107-5318-1
US-08-477-5318-1
US-08-477-728-47
US-08-477-728-47
US-08-477-728-47
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REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 63, Application US/07634278
Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Town
STRET: 379 Lytton Avenue
CTTY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: QUEEN, Cary L.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-07-634-278-63
                                               441
438
434
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432.5
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87.531 Million cell updates/sec
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Sequence 87,
Sequence 63,
Sequence 87,
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Sequence 6, A
Sequence 6, A
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Sequence 63,
Sequence 87,
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Sequence 87,
Sequence 10,
Sequence 10,
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                                                                                                                 October 11, 2001, 12:01:06; Search time 25.17 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                    1 EIVLTQSPATLSLSPGERAT......CQQSGSWPHTFGGGTKVEIK
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Sequence 6
Sequence 6
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PGCOMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                 Compugen Ltd
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US-08-474-040-62
US-08-487-200-62
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US-07-634-278-83
                                                                                                                                                                                                                                                                                                        197339 segs, 20590346 residues
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               GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                    US-08-791-391A-32
                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Perfect score:
Sequence:
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Result

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RESULT 3
US-08-477-728-63
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                                                                                                                                                                                                                              1. EIVLTQSPGTLSLSPGERATLSCRASQSISNNLHWYQQKPGQAPRLLIKYASQSISGIPD 60
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                                                                                                          Score 506; DB 1; Length 107;
Pred. No. 1e-40;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                             RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Nicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION PATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 87, Application US/07634278 Patent No. 5530101 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 326-2400
TELEFAN: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : LENGTH: 107 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

US-07-634-278-87
                                                                                                               Ouery Match
Best Local Similarity 90.7%;
Matches 97; Conservative
                       ; MOLECULE TYPE: peptide US-07-634-278-63
TOPOLOGY: linear
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                                                                                                                 1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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        Score 506; DB 1; Length 107; Pred. No. 1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 506; DB 1; Length 107; Pred. No. 1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                    7; Indels
                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK 107
                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: SCHOOL WILLIAM P.

APPLICANT: SELICK, HAROLD E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 42A
APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Townsend and Townsend and Crew
Two Embarcadero Center, 8th Floor
                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                    Sequence 63, Application US/08477728 Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: II
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-240
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
          90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.8%;
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Query Match
Best Local Similarity 90.79
Watches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.7*
These 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
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61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK 107

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ADDRESSEE:
      RESULT 5
US-08-474-040-63
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Pred. No. 1e-40;
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-5UN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 3-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 3-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1988
ANAME: AS DEC-1988
ANAME: AS DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPRAM: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    Sequence 87, Application US/08477728
Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.8%;
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Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide.US-08-477-728-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          94111
                                                                                                              RESULT 4
US-08-477-728-87
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Micholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                1: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 506; DB 1;
Pred. No. 1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 94301
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 63, Application US/08474040 Patent No. 5693761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.8
Best Local Similarity 90.7
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-474-040-63
                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
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RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107

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CO, Man Sung SCHNEIDER, William

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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVLTQSPGTLSLSPGERATLSCRASQSISNNLHWYQQKPGQAPRLLIKYASQSISGIPD 60
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Pred. No. 1e-40;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK 107
                                               APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Nicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
APPLICANT: COELINGH COELINGH CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFCATION 546
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 310,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2400
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
Sequence 87, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/08487200
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                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and TC
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 90.7
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 COUNTRY: CZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-487-200-63
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
ATTLE OF INVENTION: MRROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                   Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PULGASJITICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

FILING DATE: 18-FEB-1989

PRIOR APPLICATION DATA:

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

FILING DATE: 18-FEB-1989

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY AGENT INFORMATION:

NAME: Smith, William M

REFERENCE/DOCKET NUMBER: 11823-002610

TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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; Patent No. 5693762
; GENERAL INFORMATION:
                                                                                                                                 LOWINGER: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 326-2400
                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.83
Best Local Similarity 90.73
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-487-200-63
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                        ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-487-200-87
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US-08-484-537-63
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Pred. No. 1e-40;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK 107
                  APPLICANT: CO, Man Sung
APPLICANT: CCHNELDER, William P.
APPLICANT: SCHUREDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, HAROLDE E.
APPLICANT: SELICK, HAROLDE E.
TITLE OF INFENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSENG and TOWNSENG and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11823-002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALON AFFLLON DAMER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION UNMER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH WILLIAM M
REGISTRATION NUMBER: 11823-00261
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/487,200 FILING DATE: 7-40N-1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/08484537
Patent No. 6180370;
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.8%;
90.7%;
QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.87
Best Local Similarity 90.77
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-484-537-63
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                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SCLICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
COUNTRY: US
ZIP: 94301
COMPUTED TO THE COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 107;
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90.7%; Pred. No. 1e-40;
iive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISKLEPEDFAVYCQQSNSWPHTFGQGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278 %
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-EB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLEI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.8'
Best Local Similarity 90.7'
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: No. 6066718artis Patent and Trademark Department STRET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.2%; Score 480; DB 2; Length 127; 85.0%; Pred. No. 3.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                              OPERATING STSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/127,721A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INPORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTONING DATE: 25-SEPTEMBER-1992
ATTONING DATE: 18-08045, Henry P.
NAME: NO. 5958708AX, Henry P.
REGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08127721A Patent No. 6066718 GENERAL INFORMATION:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 85.0
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-476-1768-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
       59 Route 10
                         East Hanover
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                 ZIP: 07936-1080
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                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-127-721A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                            CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Grainger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 506; DB 4; Length 107;
Pred. No. 1e-40;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISRLEPEDFAVY/CQQSNSWPHTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOCLOBLINS
HUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1:25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 5958708artis Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTANTON UNDBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR PAPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/290,975
FILING DATE: 114-22
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.8%;
Best Local Similarity 90.7%;
Matches 97; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-484-537-87
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-476-176B-10
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha.
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STREET: New Jersey
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 18 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGRIT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPAX: (908) 277-5110
TELEPAX: (908) 277-5110
TELEPAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                              86.2%; Score 480; DB 3;
85.0%; Pred. No. 3.2e-38;
tive 7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-476-176B-6
Sequence 6, Application US/08476176B
Patent No. 5958708
     INFORMATION FOR SEQ ID NO: 10:
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                                        : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.1
Best Local Similarity 83.2
Matches 89; Conservative
                                                                                                                                                                                                  Conservative
                       SEQUENCE CHARACTERISTICS
                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-246A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-1768-6
                                                                                                                                                              Query Match
Best Local Similarity
Matches 91; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVLTQSPGTLSLSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE PORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127/721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 05 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 607203364, Henry P.
REGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (908) 277-5110
(908) 277-4306
                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 85.0 Matches 91; Conservative
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                             ; MOLECULE TIPE
US-08-127-721A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-485-246A-10
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21 DILLTQSPGTLSLSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLIKYASESISGIPS 80
1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                Sequence 6, Application US/08127721A

Sequence 6, Application US/08127721A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Saldamna, Jose
TITLE OF INVENTION: immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
STREET: 59 ROULE 10
CITY: East Hanover
STREET: New Jersey
COUNTRY: USA
COUNTRY: USA
COMPTER READABLE FORM:
                                                                                       OPERATING SISTEM: rc.Dos/ma-los
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066/18ak, Henry P.
REGISTRATION NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 2777-5110
TELEPHONE: (908) 2777-4306
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERICATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-127-721A-6
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ö Gaps ; 0 Query Match 85.1%; Score 474; DB 3; Length 127; Best Local Similarity 83.2%; Pred. No. 1.2e-37; Matches 89; Conservative 9; Mismatches 9; Indels

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Search_completed: October 11, 2001, 12:01:06 Job time; 916 sec

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-0.70

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46

0

0.71

351

351

Release 5.4

100-

```
Sequence 1, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Init. Opt.
Length Score Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Significance
Mismatches
                                                                                                                                                          US-08-791-391A-1 (1-351)
US-08-790-540A-1 Sequence 1, Application US/08790540A
   351
                                                                                                                321
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score = 351
Matches = 351
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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1. US-08-790-540A-1 Sequence 1, Application
                                                                                                            2. US-08-790-540A-3 Sequence 3, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-IX 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-IX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELERAX: (619) 535-9001
TELERAX: (619) 535-9001
TELERAX: (619) 535-9001
TELERAX: (619) 535-901
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                                The list of other best scores is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
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                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 11 11
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
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Residue Identity
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                               Sequence Name
                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                          made by jdelaval on Thu 11 Oct 101 12:15:05-PDT
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Length Score Score Sig. Frame
                                                                                                                                                                                                                       Results of the initial comparison of US-08-791-391A-1 (1-351) with: File : 08-790540.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
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32
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                                                                                                                                                       Ouery sequence being compared:US-08-791-391A-1 (1-351)
Number of sequences searched:
Number of scores above cutoff:
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Joining penalty
Window size
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                                                              FastDB - Fast Pairwise Comparison of Sequences
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47
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                                                                                                            Results file us-08-791-391a-1.res
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00:00:00.00
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0.33
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Number of sequences searched:
Number of scores above cutoff:
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198
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               IntelliGenetics
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Gap size penalty
Cutoff score
Randomization group
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Similarity matrix Mismatch penalty

Scores:

Times:

Sequence Name

39-

SCORE 0

0.71 . .

180

170

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Sequence 3, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
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TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION HUMAN
TITLE OF INVENTIO
Optimized Score = 100 Significance = -0.70 Matches = 125 Mismatches = 87 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                       ADDITION OF THE CALLED TO STREET: 43.0.
CITY: San Diego
STATE: California
COUNTRY: United States
2.1P: 92.12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/790,540A
FILING DATE: 30-JAN-1997
FILING DATE: 30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-791-391A-1 (1-351)
US-08-790-540A-3 Sequence 3, Application US/08790540A
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELEPHONE: (619) 535-9901
TELEPHORE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46
488
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80

9

100

90

GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACTCTTTCCTGCCAG

Sig. Frame

-0.71

o

0.71

117

Release 5.4

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Sequence 2, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 117 Significance = Matches = 117 Mismatches = Conservative Substitutions = =
                                                                               Init. Opt.
Length Score Score
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GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
                                                                                                                                         σ
      117
                                                                                                                                                                                            1. US-08-791-391A-2 (1-117)
US-08-790-540A-2 Sequence 2, Application US/08790540A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-791-391A-2 (1-117)
US-08-790-540A-4 Sequence 4, Application US/08790540A
    117
                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                           RUDKESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 90 110 X
DNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. US-08-790-540A-2 Sequence 2, Application U
                                                                                                                                     2. US-08-790-540A-4 Sequence 4, Application U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-IX 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8049
INPORMATION FOR SEQ ID NO: 2:
                                        The list of other best scores is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States
                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                    Sequence Name
                                                                                                                                     Results file us-08-791-391a-2.res made by jdelaval on Thu 11 Oct 101 12:13:43-PDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Init. Opt.
Length Score Score Sig. Frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Standard Deviation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A 100% identical sequence to the query sequence was found:
                                                                                                                                                                                            Query sequence being compared:US-08-791-391A-2 (1-117)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.37
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Joining penalty
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                                                                             FastDB - Fast Pairwise Comparison of Sequences
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00:00:00.00
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Number of sequences searched:
Number of scores above cutoff:
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63
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Gap penalty
Gap size penalty
Cutoff score
Randomization group
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Similarity matrix Mismatch penalty

SCORE

NECZECOES

Scores:

Times:

Sequence Name

0.71

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TITLE OF INTERPRIORS AND ANTIDODIES, NUCLEIC Acids Encoding Same and Methods of Use CORRESPONDENCES. 14 CORRESPONDENCES. 14 CORRESPONDENCE ADDRESS. 14 CORRESPONDENCE ADDRESS. 15 CORRESPONDENCE ADDRESS. 15 CORRESPONDENCE ADDRESS. 15 CORPUTER. 1470 La 2011 VILLAGE DELIVE, SULTE 700 CONTREY. 15 CORPUTER. TEADABLE FORM. 15 CORPUTER. THAN FOR COMPANIAN SYSTEM: PC-DOS/MS-DOS CORPUTER. 18 PC-CORPUTER. 18 PC-CORPUTER.
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0.71

320 23

321

Release 5.4

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Sequence 3, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: HUSE, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES:
ADDRESSE: Campbell 6 Flores LLP
     Init. Opt.
Length Score Score Sig. Frame
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                                                                                                                        US-08-791-391A-3 (1-321)
US-08-790-540A-3 Sequence 3, Application US/08790540A
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                     E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
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                                      1. US-08-790-540A-3 Sequence 3, Application 2. US-08-790-540A-1 Sequence 1, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
'REFERENCE/DOCKET NUMBER: 9-1X 24
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 base pairs
                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320
99%
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1.321
                                                                                                                                                                                                                                                                                                                      STREET: 4370 La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                      Sequence Name
                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                    Results file us-08-791-391a-3.res made by jdelaval on Thu 11 Oct 101 12:15:41-PDT
                                                                                                                                                                                                                                                Results of the initial comparison of US-08-791-391A-3 (1-321) with: File : 08-790540.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Standard Deviation 210.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A 100% identical sequence to the query sequence was not found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total Elapsed 00:00:00.00
                                                                                                                                                                        Query sequence being compared:US-08-791-391A-3 (1-321)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-tuple
Joining penalty
Window size
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                                                                    FastDB - Fast Pairwise Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Median
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Number of sequences searched:
Number of scores above cutoff:
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171
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71-0
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Randomization group
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Similarity matrix Mismatch penalty
Gap penalty
Gap size penalty

Scores:

Times:

SCORE 0

0.71

CTCACTATCTCCAGTCTGGAGCCTGAAGATTTTGCAGTCTATTACTGTCAACAGAGAGTGGCAGCTGGCCTCAC 240

The list of best scores is:

```
GGGCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TTLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
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TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION HUMAN
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TITLE OF INVENTION HUMAN
TITLE OF INVENTION HUMAN
TITLE
10 20 30 70 70 60 70 60 70 GAGATTGTGCTAACTCAGCCCAGGAGAAAAGGGGGAGTCTTTCCTGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30.4An-1997
CLASSIFICATION: 424
ATOONEY/AGERN INPORMATION:
NAME: Campbell, Cachryn A.
REGISTRATION NUMBER: 31,815
RESERROCE/POCKEY NUMBER: 9-1X 2405
TELEFRAM: (619) 535-9001
TELEFAM: (619) 535-9001
TELEFAM: (619) 535-9001
TELEFAM: (619) 535-9001
SEQUENCE CHARACTERISTICS:
FRAMTHON FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-791-391A-3 (1-321)
US-08-790-540A-1 Sequence 1, Application US/08790540A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                       LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Results file us-08-791-391a-4.res made by jdelaval on Thu 11 Oct 101 12:14:18-PDT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
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32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85-
                                                                                                                                  Query sequence being compared:US-08-791-391A-4 (1-107)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
                                                    FastDB - Fast Pairwise Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARAMETERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unitary
1.00
0.05
0
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> 0 < 01 lo IntelliGenetics > 0 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                 Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCORE 0
STDEV
```

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolia Village Drive, Suite 700

CITY: San Libera

CONFURK: United States

ZIE: 92122

COMPURK: In United States

ZIE: 92122

COMPURK: Enloyd disk

COMPURK: In PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Releach In PC-DOS/MS-DOS

SOFTWARE: Releach In PC-DOS/MS-DOS

SOFTWARE: Releach In PROBMATION: 0.40

FILICATION NUMBER: 105/00/190,540A

APPLICATION NUMBER: 105/00/190,540A

APPLICATION NUMBER: 105/00/190,540A

CLASSIFFATION NUMBER: 11,915

REFERENCE/OCKET NUMBER: 11,915

REPERENCE/OCKET NUMBER: 11,915

REPERENCE/OCKET NUMBER: 10,100

TELECOMMUNICATION INFORMATION: 2: 5049

INFORMATION POR RED ID NO: 2: 50409

INFORMATION POR RED ID NO: 2: 50409

INFORMATION OF RED ID NO: 3: 50409

INFORMATION OF RED ID NO: 3: 50409

INFORMATION OF RED ID NO: 4: 50409

INFORMATION OF RELEASE REPRESENTED OF RESIDENT OF RESIDE
```

Sednence:

Run on:

Searched:

T. Sept.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_htg24:*
gb_htg25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                       jb_sts2:*
jb_sts3:*
jb_sy:*
                                                                                                             b_sts1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_ro2:*
gb_in4:*
gb_pr10:*
em_ba3:*
                         em_pl:*
em_ro:*
em_sts:*
  em_pat:
                                                                   em_sy:*
em_un:*
                                                                                                                                                                  un_q
                                                                                              em_vi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302.2
268.6
268.6
259.6
259.6
258.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
Ю
                                                                                              (without alignments)
2557.737 Million cell updates/sec
                                                                             October 11, 2001, 13:23:38; Search time 2122.65 Seconds
                                                                                                                                                   351
1 CAGGTGCAGCTGGAGTC......CTACAGTGACTGTTTCTAGT 351
                                                                                                                                                                                                                                                              2688314
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                 1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_htg_inv2:*
em_htg_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_htgo_hum:*
em_htgo_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_htgo_rod:*
em_htg_hum1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     htg_inv1:*
                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_htg_hum4:
                                                                                                                                    US-08-791-391A-1
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em_htg_hum6:
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gb_in2:*
gb_in3:*
gb_om:*
gb_ov:*
gb_pat1:*
gb_pat2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_ph: *
gb_pl1: *
gb_pl2: *
gb_pl3: *
gb_pl4: *
em_ba1: *
em_ba2: *
                                                                                                                                                                                                                                                                                                                                                                                                 gb_ba1:*
gb_ba2:*
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                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                         Scoring table:
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AX060780 Sequence AX060784 Sequence IO8289 Sequence 6 54336 immunoglobu E21535 Process for E21533 Process for M83724 Mouse monoc A38870 Sequence 24

S45356 E21535 E21533 MUSIGMUD2A A38870

010 100 100 100 100

AX060780 AX060784

Description

SUMMARIES

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/protein_id="CAC24890.1"
/db_xref="GI:12406165"
/translation="EVQLVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKR
LEWVAKVSSGGGSTYYLDTVQGRFTISRDNAKNTLYLQMSSLNSEDTAMYYCARHNYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 351)
Huse, W.D. and Wu.H.
Anti-g(a) v-g(p)3 recombinant human antibodies, nucleic acids encoding same and methods of use encoding same and methods of use Patent; WO 0078815-A 5 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                             61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCT 120
                                                                                                                                                                                               CCGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTAT 180
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                         9
                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGIGCAGCIGGIGGAGICTGGGGGGAGGCGTIGTGCAGCCTGGAAGGICCCTGAGACTCT 61
                                                                                                                          241 CTGCAAATGAACTCTCTGAGAGCCGAGGACACACGCGTGTATTACTGTGCAAGACATAAC
                                                                                                          1 CAGGTGCAGCTGGTGGAGTCTGGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                        181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATAC
                                                                                                                                                                                                                                                                                                                                                                                             CTGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAAC
                                                                      ö
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCTAGT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Indels
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT
                                 ; Score 351; DB 9; I; Pred. No. 1.5e-104; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 302.2; DB 9
Pred. No. 1.7e-88;
0; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .351
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AXU60784 351 bp DNA
Sequence 5 from Patent WO0078815.
AX060784
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Best Local Similarity 91.9%;
Matches 319; Conservative
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synthetic construct
artificial sequence.
1 (abses 1 to 351)
Huse, W.D. and Wu.H.
Anti-g(a) v2-g(b)37 recombinant human antibodies, nucleic acids encoding same and methods of use
Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
 AR013776 Sequence
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/db_xref="taxon:32630"
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Sequence 1 from Patent WO0078815.
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62 CCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATTC
                                     CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT
                                                                 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
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Pred. No. 2e-77;
0; Mismatches 49; Indels 0;
                                                                                                                                                       302 ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT 348
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Patent: EP 0380068-A1 6 01-AUG-1990;
Location/Qualifiers
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Seguence 6 from Patent EP 0380068.
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Zerler, B.D.
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AUTHORS
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/gene="immunoglobulin heavy chain variable"
/note="anti-human IL-2R; This sequence comes from Fig. lb"
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                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 488)
Rose, B., Gillespie, A., Wunderlich, D., Kelley, K., Dzuiba, J., Shedd, D., Cahill, K. and Zerler, B.
Differential effects of a murine and chimeric mouse/human anti-interleukin-2 receptor antibody on human T-cell proliferation Immunology 76 (3), 452-459 (1992)
    mRNA ROD 08-MAY-1993 chain variable=anti-human IL-2R [mice, mRNA
                                                                                                                                                                                                                                                             GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 115041] from the original journal article. This sequence comes from Fig. 1b.
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/partial
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                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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S45356 488 bp
immunoglobulin heavy
Partial, 488 nt].
                                                                GI:255660
                                                S45356
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RESULT E21535

RESULT S45356

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PI KYOKO TAKAHASHI,TOSHIFUMI YUKI,TOSHIRO TAKAI,TOMOYASU TSURA PC C12N15/09,C07K16/28,C12N1/19,C12R1:31), PC (C12N1/19,C12R1:84),C12P21/02/(C12N15/09,C12R1:31), PC C12R1:31)
C2 Strandedness: Double;
CC Topology: Linear;
FH Key
FT Sig peptide 34. no
                                                                         Euteleostomi;
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 761)

( kyoko, T.T. Y. and Takai, T.T.

Process for producing antibody Fas fragment with yeast Patent; JP 1999000174-A 2 06-JAN-1999;

ASAHI BREWERIES L.D. THE NIKKA WHISKY DISTILLING CO LTD, TORII PHARMACEUT CO LTD, TOMOYASU RI

OS Homo sapiens (human)

PN JP 1999000174-A/2

PD 06-JAN-1999

PF 13-JUN-1997 JP 1997171232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGCAAGGGTCTGGAGTGGGTCGCAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTATT 181
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D-region; Ig heavy chain; J-region; V-region; immunoglobulin;
immunoglobulin mu-chain; monoclonal antiidiotypic antibody.
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Mouse monoclonal antiidiotypic antibody IgM VDJ-region mRNA.
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Pred. No. 1.9e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
228 c 206 g 161
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Location/Qualifiers
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               JP 1999000174-A/2.
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CC Strandedness: Double;

CC Topology: Linear;

FH Key

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Kyoko, T. T. Y. Y. and Takai, T. T.
Kyoko, T. T. Y. Y. and Takai, T. T.
Process for producing antibody Fas fragment with yeast
Patent: JP 1999000174-A 4 06-JAN-1999;
ASAHI BREWERIES LTD, THE NIKKA WHISKY DISTILLING CO LTD, TORII
OS HOMO Sapiens (human)
PN JP 1999000174-A/4
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                 07-FEB-2001
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E21535 723 bp DNA PAT 07-FE
Process for producing antibody Fas fragment with yeast.
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/db_xref="taxon:9606"
214 c 192 g 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide 34. 99 peptide 100. 759 peptide 763. 768. 168. Location/Qualifiers
                                                                    E21535.1 GI:13023615
                                                                                     JP 1999000174-A/4.
                                                                                                        Homo sapiens.
Homo sapiens
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JOURNAL MEDLINE FEATURES

REFERENCE AUTHORS

TITLE

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Tsou.H. and Welss.M.J.
Conjugates of methyltrithio antitumor agents and intermediates for their synthesis
Patent: US 5773001-A 56 30-JUN-1998;
Location/Qualifiers
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Hamann,P.Ross, Hinman,L., Hollander,I., Holcomb,R., Hallett,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 TAGACAGTGTGAAGGGCCGATTCACCATCTCCAGAGACAGTGCCAGGAACACCCTATACC 303
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83.9%; Pred. No. 9.6e-74;
                                                                                              King, D.J., Adair, J.R. and Owens, R.J. HUMANISED ANTIBODIES DIRECTED AGAINST AS CELLIFECH LTD (GB)
Other publication AU 555894 940704
Other publication GB 2278357 941130
Other publication GB 2278357 941130
Other publication JP 7564334T 950518.
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                                                                                                                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
1099 c 118 g 108
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100 c 117 g
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AR013776.1 GI:3971230
 A38870.1 GI:2295288
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LEWVAEISSGGSYTYYPDTVTGRFTISRDNAKNTLYLEMSSLRSEDTAMYYCARDGYY
VRFAYWGQGTLVTVSA"
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                                                                              Peptide sequences from the hypervariable regions of two monoclonal anti-idiotypic antibodies against the thyrotropin (TSH) receptor are similar to TSH and inhibit TSH-increased CAMP production in FRTL-5 thyroid cells
J. Biol. Chem. 267 (9), 5977-5984 (1992)
                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                          (bases 1 to 354)
Taub,R., Hsu,J.C., Garsky,V.M., Hill,B.L., Erlanger,B.F. and Kohn,L.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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Pred. No. 3.3e-74;
0; Mismatches 47; Indels 3;
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/product="immunoglobulin mu chain"
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/db_xref="GI:197952"
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Sequence 24 from Patent W09413805.
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/organism="Mus musculus"
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/map="chromosome 6"
/cell_line="4G11"
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Pred. No. 1e-73;
0; Mismatches 56;
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Whitlow,M.D. and Filpula,D.R.
Linker and linked fusion polypeptides
Patent: US 5990275-A 15 23-NOV-1999;
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Whitlow, M.D. and Filpula, D.R.
Linker for linked fusion polypeptides
Patent: US 5856456-A 17 05-JAN-1999;
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Sequence 15 from patent
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73.3%; Score 257.4; DB 9
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iive 0; Mismatches 56
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1e-73;
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WhitLow,M.D. and Filpula,D.R.
Linker for linked fusion polypeptides
Patent: US 5856456-A 15 05-JAN-1999;
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AR027762.1 GI:5938582
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83.9%;
              Best Local Similarity 83.9
Matches 291; Conservative
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Pred. No. 1e-73;
0; Mismatches 56;
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Whitlow,M.D. and Filpula,D.R.
Linker and linked fusion polypeptides
Patent: US 5990275-A 17 23-NOV-1999;
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                                          Query Match 73.3%;
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242 IGCAAAIGAACICTCIGAGAGCCGAGGACACAGCCGIGIATIACIGIGCAAGACAIAACI 301 MUSIGVABB 348 bp mRNA ROD 27-APR-1993 Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region L09000.1 GI:197998 V-region; immunoglobulin V region; processed gene. Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA. 302 ACGCCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT 348 sequence.

Mus musculus

Was puraryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 348)

Bloom, Du. Davignon, J.-L., Retter, M.W., Shlomchik, M.J.,

Pisetsky, D. So., Cohen, P. L., Esenberg, R. A. and Clarke, S. H.

V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr 1. 348
/organism="Mus musculus"
/strain="mul/mp-lpr/lpr"
/db_xref="taxon:10090"
/cell_line="anti-Sm hybridoma 4Dl2"
/dev_stage="adult" J. Immunol. 150, 1591-1610 (1993) 93163585 /tissue_type="spleen" 87 c 102 g Location/Qualifiers

; DB 94; Length 348; Indels 57; Query Match 72.6%; Score 254.8; DB 9 Best Local Similarity 83.5%; Pred. No. 6.8e-73; Matches 289; Conservative 0; Mismatches 57

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Gaps

241 182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC 182 CAGACAGTGTGAAGGGCCGGATTCACCATCTCCAGAGACAATGCCAGGAACACCCTGTACC

ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTC 347 us-08-791-391a-1.rge

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 351)
Clarke, S.H., Staudt, L.M., Kavaler, J., Schwartz, D., Gerhard, W. U. and Weigert, M.G.
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/note="Ig H-chain VDJ-region"
/note="Ig H-chain VDJ-region"
/codon_start=1
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Pred. No. 6.8e-73;
0; Mismatches 57; Indels 0;
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/organism="Mus musculus"
/db_xref="taxon:10090"
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Matches 289; Conservative C
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Search completed: October 11, 2001, 15:09:29 Job time: 6351 sec

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UI-HF-BK0
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AW401971 UI-HF-BK0
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AA170256 ms87910.r
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 877)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BF136279
BF577496
AW402613
BF974524
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BG503730
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BG342203
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SUMMARIES
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BF663281
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AL551886
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145
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3390
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Query
Match 1
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TITLE
JOURNAL
COMMENT
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VERSION
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BF144493
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SOURCE
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Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imagel.lll.gov

Plate: LLAM9275 row: a column: 10

High quality sequence stop: 644.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="Digital" | Not1: /lab_host="Digital" | Not1: /lab_host="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1: /lab_host="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1: /lab. Site_2: Sal1; transgenic model WMT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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1 (bases 1 to 1012)
1 (hases 1 to 1012)
Nath-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AGGTGCAGCTGGTGGAGTCTGGGGGAGACTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.2%; Score 243; DB 145; Length 877; Best Local Similarity 84.8%; Pred. No. 3.8e-63; Matches 296; Conservative 0; Mismatches 50; Indels 3
                                                                                                                                                                                                                                                                                                                                                  1..877
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/strain="C2ECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4020753"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 CTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT 348
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Smail: cgapbs-r@mail.nih.gov
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uu72905.yl Soares_mouse_NMCB_bcell Mus musculus cDNA clone
IMAGE:3382089 5' similar to SW:HV58_MOUSE P18529 IG HEAVY CHAIN V
REGION 5-76 PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 494)
    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dibbrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

94 c 109 g 105 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGGTGCAGCTGGTGGAGTCTGGGGGAGCCGTTGTGCAGCCTTGAAAGGTCCCTGAGACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 236.8; DB 149; Length 404;
Pred. No. 2.4e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                1. .404
/organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Lu29"
                                                                                                                                                                                                                                                                                                                          Seq primer: -40RP from Glbco
High quality sequence stop: 399.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:3675897"
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Best Local Similarity 87.5%;
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 bp
                                                Unpublished (1997)
                          Tumor Gene Index
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                                                JOURNAL
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                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C2ECH II"
/db_ref="texon:10090"
/clone_lib="NcI_CGAP_Lu30"
/clone_lib="NcI_CGAP_Lu30"
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/lab_host="buth108"
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/note="Organ: lung; Vector: pCNV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCNV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector model WNT-1, expression driven by
/mMTV-LTR enhancer; cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
73 a 271 c 267 g 201 t
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                   Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NGI-CGAP clone distribution information can k

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9279 row: h column: 12

High quality sequence stop: 711.

Location/Qualifiers

1. 1012
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Subaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 404)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AGGIGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCGGAAACTCT 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 238.8; DB 145; Length 1012;
Pred. No. 7.5e-62;
0; Mismatches 67; Indels 0;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 80.6%;
Matches 279; Conservative
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Murinae; Mus

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TITLE

COMMENT

FEATURES

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/organism="Mus musculus"
/strain="FVBN"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:4224109"
/clone=lib="WOI_CGAP_CO24"
/lab_host="DH10B (TI phage-resistant)"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 886)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                        1 (bases 1 to 774)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.

Bmail: capabbs-remail.nih.gov.

Tissue Procurement: Jeffery E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov.
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      Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 234.6; DB 1
Pred. No. 1.3e-60;
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High quality sequence stop: 675.
Location/Qualifiers
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BF582912.1 GI:11656630
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86.9%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                Tumor Gene Index
Unpublished (1997)
Other_ESTS: uu72905.x1
Other_ESTS: uu72905.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Conscrium (info@image.llnl.gov) for further information. MGI: L087085
Seq primer: -40RP from Gibco
High quality sequence stop: 471.
Location/Qualifiers
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 CCTGTGCAGCCTCTGGATTCACTTTCAGTACCTATGGCATGTCTTGGGTTCGCCAGACTC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CGGCCAAGGCTCTGGAGTGGGTCGCAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 CAGACAAGAGGCTGGAGTGGGTCGCAACCATTAGTAGTGGTGATAGTTACACCTACTATC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACA---- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 AGGTGCAGCTGGTGGAGGTCTGGGGGAGACTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGGIGCAGCIGGIGGAGICTGGGGGGGGGGGTGTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 174; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 TAACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 236.6; DB 174; Lengt
Pred. No. 2.9e-61;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 t
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3382089"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF581450.1 GI:11655162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.4%;
Best Local Similarity 81.8%;
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 c
                                                                                                                                                                                                                                                                                                                                                                          1. .494
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house mouse.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF581450
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
BF581450
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KEYWORDS
SOURCE
                                                                                  JOURNAL
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Gaps 61

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Indels

39;

DB 150; Length 774;

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/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="Hous"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note:"/note: pt/T3D-Pac (Pharmacia) with a modified
/note: pt/T3D-Pac (Phar
                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMGE Consortium (info@lmage.lln!gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
   Schurk, R., Ritter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA170256 823 bp mRNA EST 16-FEB-1997 ms87g10.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:618594 5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 CAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAGGAACACCCTGTACC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                         Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGGTGCAGCTGGTGGAGTCTGGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:618594"
/clone_lib="Soares mouse 3NbMS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 230.4; DB 2
Pred. No. 2.2e-59;
0; Mismatches 41
                                                                                          The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.6%;
Best Local Similarity 86.1%;
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct orientation)
MGI:379418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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DEFINITION
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ORIGIN
                                                                                             TITLE
JOURNAL
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AA170256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/dlone="InAGE:4224494"
/clone="InAGE:4224494"
/clone="InAGE:4224494"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_9: Site_1: site_1: 6 kb. Constructed by iife
Average insert size 1.6 kb. Constructed by iife
Technologies. Note: this is a NCI_CGAP Library."
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5' similar to gb:x14584 IG HEAVY CHAIN PRECURSOR v-III REGION
HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy
chain V region mRNA, (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 4by)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.

Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 469)
                                                                                                                                                                                          þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 CGGAGAAGAGGCTGGAGTGGGTCGCAACCATTAGTAATAGTGGTTATGCTACCCACTATC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 CAGACAGTATGAAGGGGCGATTCACCATCTCCAGAGACAATGCCCAGAACACGGTGTTAC 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AGGTGCAGCTGGTGGAGTCTGGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61
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                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://mage.lln.gov
http://mage.lln.gov
http://mage.lln.gov
icolanipi.gov
http://mage.lln.gov
icolanipi.gov
light
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                              Email: cgapbs-r@mail.nih.gov
Thsue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 150; Length 886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 ACTGGTACTTCGATGTCTGGGCGCGCAGGGACCACGGTCACCGTCTC 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                        .886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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BF579001 650 bp mRNA EST 12-DEC-2000 602096117F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4215844 5',
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/dclone="lnAGE:4218844"
/clone=lib="NLICGAR-CO24"
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/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: phage-resistant"
// Rechnologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Confact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM9792 row: b column: 05
High quality sequence stop: 649.
299 CAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAGGAACACCCTGTACC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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                                                                                         242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACAT
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Pred. No. 3.2e-59;
0; Mismatches 60;
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11 Similarity 81.2%;
281; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Ten,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE_Consortium (info@lmage.llnl.gov) for further information.
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(HUMAN); gb:V00821 Mouse mRNA fragment for immunoglobulin muencoding the C-terminus (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Conteact: Marra M.Mouse EST Project
WashIU-HHMI Mouse EST Project
WashIngton University School of MedicineP
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MG1:379418
Putative full length read
Vector to vector length is 867
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:618594"
                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
                                                                 AA170256.1 GI:1748794
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                                                                                                                                     Mus musculus
                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                     Waterston, R.
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Matches
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                                            ACCESSION
                                                               VERSION
KEYWORDS
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DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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Anote—Organ: lung; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                               BF138708 1559 bp mRNA EST 24-OCT-2000 601781893F1 NCI_CGAP_Lu30 Mus musculus CDNA clone IMAGE:4009847 5',
                                                290 CAGACAGTGTGAAGGGGGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTTCC 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:4009847"
/clone=lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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Pred. No. 9.2e-59;
0; Mismatches 62; Indels
                                                                                                                                                                                                 302 ACGCCAGTTTTGCTTACTGGGGCCCAAGGGACTACAGTGACTGTTTC 347
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/strain="CZECH II"
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80.1%;
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Best Local Similarity 80.1:
Matches 285; Conservative
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/clone_lib="NIH_MGC_36"
/fissue_type="lymph"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="germinal"
/cell_type="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 406)

I (Dases 1 to 406)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Ewail: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CONA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAL at:

www-bio.lnl.gov/bbrp/image/image.html

Seq primer: MI Stoares Lab

Contact: Mammalian at:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGAGGGTCCCTGAGACTCT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                             AW401971 406 bp mRNA EST 16-FEB-2000 UI-HF-BKO-aao-c-04-0-UI.rl NIH_MGC_36 Homo sapiens CDNA clone IMAGE:3054342 5', mRNA sequence.
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                                                                        302 ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTC 347
                                                                                                                ATCTGACTATGGGGTCAAGGAACCTCAGTCTC 469
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/db_xref="taxon:9606"
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Gaps 61

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AW824857 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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293 CAGACACAGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTTCC 352
                                                                                                                                                                      242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGAC---ATA 298
 122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGTAGCACCTACTATT 181
                      182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
                                                                                                                                                                                                                     mRNA sequence.
BF143948
BF143948.1 GI:10982988
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                   AW824857 454 bp mRNA EST 17-MAY-2000 us08c01.yl Soares_NMGBC_B-cell Mus musculus cDNA clone IMAGE:3166464 5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR -II REGION (HUMAN); gb:U33089 Mus musculus CBl7 SCID immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 454)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                    409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACA---- 296
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                    410 TATGGCCCTTTAGGGGGTTTGCTTACTGTGGCCAAGGGACTCTGGTCACTGTCTTT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.1%; Score 228.4; DB 121; Length 454; 81.3%; Pred. No. 8.8e-59;
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                                                                      297 ----TAACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40RP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
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Best Local Similarity 81.3
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                   house mouse.
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FEATURES

BASE COUNT

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/organism="Mus musculus"
/strain="CZECH II"
/db_refe"taxon:10090"
/clone="InAGE:401440"
/clone_lib="NcI_CGAP_Lu30"
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/lab_host="bullos"
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Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

13 a 236 c 236 g 176 t lothers
BF143948 862 bp mRNA EST 24-OCT-2000 601786493F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014430 5',
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80.4%; Pred. No. 1.6e-58;
iive 0; Mismatches 67;
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ESM Mus musculus:

ENARYOTA: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;

Musmania: Eutheria, Rodentia: Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 718)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Enals: capabs-rémail.nih.gov

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-C&P clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 671.

High quality sequence stop: 671.
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/clone="IMAGE:4009197"
/clone="IMAGE:4009197"
/clone="IMAGE:4009197"
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/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/not1; clone="Organ: lung; Vector: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF136279 718 bp mRNA EST 24-OCT-2000 601780988F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009197
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                                                                                                                                                                                                                                     240 CAGGGAAGGGCTGGAGTGGGTTCATACATACATAGTAGTGGTAGTACTACCATATACTACG
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/strain="CZECH II"
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//organism="Homo sapiens"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone="IMAGE:3056371"
//clone="IMAGE:3056371"
//clol=llp="mult=MAGC_36"
//tissue_type="germinal center B cells"
//cell_type="germinal center B cells"
//lab_host="BH108 [LTI]"
//oot="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
//oot="Vector: pT7T3-Pac; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
Cloe distribution: MGC clone distribution information can be found through the I.M. NGC.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: MJS Porward.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 440)
                                                                                                                                     220 CAGAGAAGGGCTGGAGTGGGTTGCATAGTAGTGGCAGTAGTACCATCTACTATG 279
                                                                                                                                                                                                                                                                                                                   280 CAGACACAGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTTCC 339
160 CCTGTGCAGCCTCTGGATTCACTTTCAGTGACTATGGAATGCACTGGGTTCGTCAGGCTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW408304 440 bp mRNA EST 16-FEB-2000 UI-HF-BK0-abj-e-10-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056371 5', mRNA sequence.
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                                                                                       122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT
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TITLE JOURNAL

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FEATURES

REFERENCE AUTHORS

Search completed: October 11, 2001, 14:33:59 Job time: 5536 sec THIS PAGE BLANK (USPTO)

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(IXSY-) IXSYS INC
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                                                                                                                                                                                                              1 CAGGTGCAGCTGGTGGAGTC......CTACAGTGACTGTTTCTAGT 351
                                                                                                         ; Search time 177.65 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     730101 seqs, 313950809 residues
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                                                                                                       October 11, 2001, 13:24:48
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Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta_3. The diagnosis and treatment of alphavbeta_3. The diagnosis and chronic articular rheumatism), discases (such as psoriasis and chronic articular rheumatism), discorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Raposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
                                                                                                                                   (MOLE-) APPLIED MOLECULAR EVOLUTION
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 132pp; English.
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Matches 351; Conservative
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                                                                                                     Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
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100.0%; Pred. No. 9.9e-100;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                 Claim 3; Fig la; 129pp; English.
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                                         WPI; 1998-437472/37
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Length 351;
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100.0%; Score 351; DB 22; 100.0%; Pred. No. 9.9e-100;
                                                      0; Mismatches
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Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; anglogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LM609 and the antibody vitaxin bind selectively to integrin alphavbetas and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non )immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                               /product= "LM609 antibody heavy chain variable region" /note= "partial sequence, no start or stop codon given"
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Pred. No. 1.5e-84;
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ilarity 91.9%;
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), diseases (such as psoriasis and chronic articular rheumatism) vessels (such as diabetic retinoporphy, neovascular glaucoma and cancer disorders such as tumnours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 aagtgcagctggtggagtctggggggggggcttagtgaaggcctggaaggtccctgagactct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGTGCGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cctgtgcagcctctggattcgctttcagtagctatgacatgtcttgggttcgccagattc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCCAAGGCTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTACCACTACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 351;
                                                                                                                                                                                                                                      grafted antibody; alphaVbeta_3 integrin; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                inflammatory; cancer; retina; restenosis; osteoporosis;
ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..5e-84;
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 A; 81 C; 102 G; 85 T; 0 other;
                                                                                                                                                                                                       Antibody LM609 heavy chain variable region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.1%; Score 302.2;
llarity 91.9%; Pred. No. 1.5e
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) APPLIED MOLECULAR EVOLUTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 132pp; English.
                                                                                                           ВÞ
                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000WO-US17454.
                                                                                                          AAF28177 standard; DNA; 351
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0339922
                                                                                                                                                                         (first entry)
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les 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 351 BP;
                                                                                                                                                                                                                                                                                                                 WO200078815-A1
                                                                                                                                                                                                                                                                                     Unidentified.
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                                                                                                                                                                         03-APR-2001
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Best Local S
Matches 319
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302
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313 cagacactgtgaagggccgattcaccatctccagagacaatgccaagaacacctttacc 372
                                                                                                   Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human mammary fat globule; human breast carcinoma; murine anti-HWFG monoclonal antibody KC-4; humanised analogue; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence encodes a humanised murine anti-human carcinoma antibody heavy chain variable region. The humanised antibody is useful for carcinoma therapy and diagnosis and for in vivo imaging of neoplastic cells. It is also of use in inhibiting the growth of a primary or metastasised neoplasm.
                                                                                    242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT
                                                                                                                                                                                                                                                                                                  Humanised murine KC-4 immunoglobulin heavy chain V-region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New analogue peptide(s) comprising antibody variable regions used to develop prods. for use in the detection, diagnosis, therapy and prevention of neoplasms
                                                                                                                                    Peterson JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           58..416
/*tag- b
/product- heavy_chain_V-region
/forced_thumanised framework region
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                                                                                                                                                                                                                                                                                                                                                                                                                                        a
"humanised KC-4 VH chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Do Couto FJR, Padlan EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CANC-) CANCER RES FUND CONTRA COSTA.
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                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                          BP.
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93US-0129930.
93US-0134346.
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                                                                                                                                                                                                                                                                                                                                                                          Chimeric Mus musculus. Chimeric Homo sapiens.
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08-OCT-1993;
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                                                             122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTGCAGCTGGTGGAGTCTGGGGGGGGGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADS comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MADS, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
            TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAAACACCCTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                                                                                                                                                                                                             Sequence encoding variable region of murine AHT 54 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                     Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 482;
                                                                                               302 ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT 348
                                                                                                             302 acggcagttttgcttactggggccaagggactctggtcactgtctct 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;
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0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.5%; Score 268.6;
85.9%; Pred. No. 4.6
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
75..482
                                                                                                                                                                                    AAQ05555 standard; DNA; 482 BP.
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Best Local Similarity 85.99
Matches 298; Conservative
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24-JAN-1989;
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182
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Homo sapiens.
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                                                      CCTGTGCGGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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                                                                                                                                                                   239 aagacactgtgacgggccgattcaccatctccagagacaattccaagaacaccctgtacc 298
                                                                                                    cctgtgcagcctctggattcgctttcagtagctatgccatgtcttgggttcgccaggctc 178
                                                                                                                                                                                              242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
                                                                                                                                                                                                                tgcaaatgaacagtctgagggctgaggacacggccgtgtattactgtgcaagggaggact 358
                           Gaps
                                             61
                                                                                                                                                                                                                                  ACGG------CAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCTAGT 351
                                                                                                                                                                                                                                            New humanised anti-KC-4 monoclonal antibody - used for detection of cancer cells, in vivo imaging, ex-vivo purging and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybridomas were prepd. based on the anti-KC-4 mouse hybridoma ATCC HB 8710 (US4708930). The murine variable regions were modified at particular AAs by PCR to provide humanised sequences. The anti-KC-4 humanised DNA sequences for the VH and VL segments are shown in
                                                                                                                     CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT
                                             AGGTGCAGCTGGTGGAGTCTGGGGGGGGGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                          TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACATAGTAAGAACACCCTATACC
                          6
         Length 417;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                             Anti-KC-4 antibody; humanised antibody; cancer; ss.
       DB 15;
                  .4e-72;
       Score 263.8; D
Pred. No. 1.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Table 22, Page 46; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
                                                                                                                                                                                                                                                                                                                                                          Humanised anti-KC-4 antibody VH FR-HZ
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                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..417
/*tag= a
                                                                                                                                                                                                                                                                                                    BP.
       75.2%;
85.8%;
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                          308; Conservative
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                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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         Query Match
                   Local
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                  Best Loca
Matches
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239 aagacactgtgacgggccgattcaccatctccagagacaattccaagaacaccctgtacc 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 TAGACACTGTGCAGGGCCGATTCACCATCTCCCAGAGACAATAGTAAGAACACCCTATACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 TGCAAATGAACTCTCTGAGAGCGGAGACACAGGCGTGTATTACTGTGCAAGACATAACT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 tgcaaatgaacagtctgagggctgaggacacggccgtgtattactgtgcaagggaggact 358
                                                                                                                                                                                                                                                                                                                                                                    Gaps
AAQ87534 and AAQ87533 respectively. Plasmid constructions comprising the humanised variable regions and the human constant regions were then used to transfrom SSP2/0-Ag14 myeloma cells to produce the humanised anti-KC-4 MAbs. The deduced As sequences of the humanised anti-KC-4 variable light and heavy chains are given in
                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity determining region; CDR; murine; mouse; human; high affinity; immunoglobulin E; receptor; monoclonal antibody; IgE; MAD; heavy chain; variable region; humanised; semi-chimeric; chimeric; treatment; prevention; disease; allergy; CRA2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 ACGG------CAGITITIGCITACTGGGGCCCAAGGGACTACAGTGACTGTTTCTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding heavy chain variable region of human CRA2 antibody.
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                                                                                                                                                                                                                                                                                                            Length 417;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                               Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                      Score 263.8; DB 16;
Pred. No. 1.4e-72;
0; Mismatches 42;
                                                                                                                                                        AAR70470 and AAR70471 respectively.
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                                                                                                                                                                                                                                                                                                      75.2%;
ilarity 85.8%;
Conservative
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(NIKK-) NIKKA WHISKEY KK.
(TORI ) TORII YAKUHIN KK.
(TSUR/) TSURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0024816.
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 308; Conserv
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97JP-0171232

us-08-791-391a-1.rng

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13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX01216;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AntiFc epsilon RI alpha chain antibody; antibody production; human; ds
                                                                                                                                                                                                                                               CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                          tgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagacataatt 519
                                                                                                                                                                                                                                     CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                      TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
                                                                                                                                                                                                61
                                   The present sequence, which encodes the heavy chain variable region of the human antibody (Ab) CRA2, was used in the preparation of a humanised or semi-chimeric monoclonal Ab (MAb), comprising complementarity determining regions (CDR) from a murine, anti-human high affinity immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric or chimeric MAb can be used to treat or prevent diseases, specifically allergies, associated with the receptor, and has very low antigenicity in humans.
                                                                                                                                                                                               AGGTGCAGCTGGTGGAGTCTGGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                             cagggaaggggctggagtgggtggccttcattagtaatcgtggtggtagcacctactatc
                                                                                                                                                                                                                                                                                                               TAGACACTGTGCAGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human antiFc epsilon RI alpha chain antibody coding sequence #2.
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                                                                                                                                                         DB 18; Length 582;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                          ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTC 347
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 582 BP; 133 A; 134 C; 155 G; 160 T; 0 other;
                                                                                                                                                        Score 259.6; DB 18;
Pred. No. 3.1e-71;
); Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers 34..753 /*tag= a 34..90
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX01214 standard; cDNA to mRNA; 761
                   Disclosure; Fig 9; 26pp; Japanese.
                                                                                                                                                                            ó
                                                                                                                                                       74.0%;
llarity 84.4%;
Conservative (
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91..750
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antigenicity in humans
                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , 13-JUN-1997;
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                                                                                                                                                       Query Match
Best Local Simi
Matches 292;
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This sequence encodes a human antife epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast Pichia pastoris as the host cell. The method can prepare an antibody Fab fragment cost efficiently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 cagacactgtaaagggccgattcaccatctccagagacaacgccaagaactcactgtatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 cagggaaggggctggagtgggtggccttcattagtaatcgtggtggtagcacctactatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human antiFc epsilon RI alpha chain antibody coding sequence #4
                                                                                                                                                                                                       Preparing an antibody Fab fragment using yeast - in high yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%; Score 259.6; DB 20; Length llarity 84.4%; Pred. No. 3.4e-71; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 ACGGCAGTTTTGCTTACTGGGCCCAAGGGACTACAGTGACTGTTTC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 761 BP; 166 A; 228 C; 206 G; 161 T; 0 other;
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3.762

34.795

34.99

/*tag= b

100.759

/*tag= c
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     BREWERIES LTD.
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                         NIKKA WHISKEY KK
TORII YAKUHIN KK
                                                                                                                            WPI; 1999-124394/11.
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nes 292; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            in high yield.
                                                                             (TSUR/) TSURA T.
                                                                                                                                                   P-PSDB; AAW73874
(ASAK ) ASAHI H
(NIKK-) NIKKA W
(TORI ) TORII M
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10-DEC-1993;
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22-JUL-1993;
                                                                           primer_bind
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                                                                                                                                                                                                                                                                              This sequence encodes a human antiFc epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast Pichia pastoris as the host cell. The method can prepare an antibody Fab fragment cost efficiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 aggigcagciggiggagicigggggaggciiggiccagccigggggggiccigagacici 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 259.6; DB 20; Length 770;
Pred. No. 3.4e-71;
); Mismatches 54; Indels 0;
                                                                                                                                                                                                                           Preparing an antibody Fab fragment using yeast - in high yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 ACGGCAGTITIGCITACTGGGGCCAAGGGACTACAGTGACTGTTTC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 atggaggaatggactactgggggcaagggaccacggtcaccgtctc 446
                                                                                                                                                                                                                                                                                                                                                           Sequence 770 BP; 172 A; 223 C; 205 G; 170 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAb A33 heavy chain coding sequence.
                                                                                                                                                                                                                                                   Claim 6; Page 9-10; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ68650 standard; DNA; 413 BP
                                                                                                                                                                                                                                                                                                                                                                                                     74.0%;
84.4%;
                                                                                                               (ASAK ) ASAHI BREWERIES LTD.
(NIKK-) NIKKA WHISKEY KK.
(TORI ) TORII YAKUHIN KK.
                                                              97JP-0171232
                                                                                        97JP-0171232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 84.4
Matches 292; Conservative
                                                                                                                                                                                    WPI; 1999-124394/11.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                    in high yield.
                                                                                                                                                                                                  P-PSDB; AAW73876
                                                                                                                                                         (TSUR/) TSURA T.
        JP11000174-A.
                                                                                        13-JUN-1997;
                                                             13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-1995
                                    06-JAN-1999.
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The sequences given in AAQ68649-50 encode the light and heavy chain variable regions (VH and VL) of the humanised anti-A33 antibody of the invention. These fragments were produced by PCR using the primer sequences given in AAQ68624-48. The amplified fragments were used in the construction of vectors for the expression and secretion of the chimeric humanised A33. The amplified products were cleaved with BstBI and SplI for the light chain and HindIII and ApaI for the heavy chain. These fragments were cloned into the human kappa light chain acceptor vector, pMRRI51, and the human heavy chain, IgG1; acceptor vector, pMRRI51, and the human heavy chain. Proteins which bind the A33 antigen can be used in the diagnosis or treatment of colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 aagtgaagctggtggagtctggggggggggcttagtgaagcctggagggtccctgaaactct 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibodies raised against A33 antigen – are used for diagnosis or treatment of colorectal tumours and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15; Length 413;
colorectal cancer; metastases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.3%; Score 257.4; DB 15; Length
83.9%; Pred. No. 1.3e-70;
Live 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 3(ii); 90pp; English.
                                                                                                                                 Location/Qualifiers
antigen; diagnosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ξ,
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93GB-0015249.
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396..413
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                                             Chimeric - Mus musculus.
Chimeric - Homo sapiens.
                                                                                                                                                           1..32
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLLT ) CELLTECH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adair JR, King DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-217881/26.
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Gaps

0;

Length

241

604

348

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particularly used to prepare single chain antibody FV fragments (scFV), potentially useful for diagnosis and treatment of cancer. The fusion polypeptide containing the specified linkers is proteolytically stable (associated with positioning of the P residue) and resistant to aggregation, while residue X improves solubility. The present sequence represents the nucleotide sequence of a A33/212 scFV fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; linker; linked fusion polypeptide; multichain protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide linkers, linked fusion polypeptides containing the linkers and
                                                                                                                                                                                                              62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                          122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                               605 tgcaaatgagcagtctgaggtctgaggacacggccttgtattactgtgcaccgactacgg 664
                                                                                                                                                                                                                                                                                                                                                                                         545 tagacagtgtgaagggccgattcaccatctccagagacagtgccaggaacaccctatacc
                                                                                                                                                                                                                                                                                                                       242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGGCCGTGTATTACTGTGCAAGACATAACT
                                                                                                                                                                                                 2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                               TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
                                                                                                                                 Score 257.4; DB 20; Leuy...
Pred. No. 1.6e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT
                                                                                                  Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linked fusion protein A33/212 sFv coding sequence.
                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein complex; antibody; ss
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92US-0980529.
93US-0002845.
                                                                                                                                          Query Match 73.3%;
Best Local Similarity 83.9%;
Matches 291; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ENZO-) ENZON
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20-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ37397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention is directed to a novel peptide linker useful for connecting polypeptide constituents into a novel linked fusion polypeptide. The polypeptide constituents into a novel linked fusion polypeptide. The peptide linker includes at least one XP motif (where X is a charged amino acid) and includes any of these sequences (GSYSGSXPGSGSCBSTKG; GTSGSGXPGSGSCBCSTKG; or GTSGKSEGKG) to inhibit its proteolysis by subtilisin or trypsin. DNA molecules encoding fusion polypeptides, containing two polypeptides, derived from the same multichain protein of the immunoglobulin (Ig) superfamily and a peptide linker as above, are
    244 tagacagtgtgaagggccgattcaccatctccagagacagtgccaggaacaccctatacc 303
                            242 TGCAAATGAACTCTCTGAGAGCCGAGGACACACGTGTATTACTGTGCAAGACATAACT 301
                                                        304 tgcaaatgagcagtctgaggtctgaggacacggccttgtattactgtgcaccgactacgg 363
                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                            SCFV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding fusion polypeptide including protease resistant linker or making single-chain Fv antibody fragments, e.g for diagnosis treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for peptide linker 212"
                                                                                                                                                                                                                                                                                            Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; multichain protein; immunoglobulin; single chain antibody Fv; aggregation; ds.
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"sequence coding for A33 Vl region"
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/note= "sequence coding for A33 Vh region"
                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "the start codon is not indicated"
                                                                                "A33/212 scFv"
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/note= "sequence coding
364..708
                                                                                                                                                                                                                                                                  A33/212 single-chain Fv coding sequence.
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/*tag=
/note=
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P-PSDB; AAW95440.
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15-JAN-1993;
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Query Match
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                        This sequence encodes a linked fusion protein containing the amino acid linker of the invention. The linkers are used for connecting constituent polypeptides to form novel linked fusion polypeptides. Polypeptides derived from any protein can be connected, in particular multichain protein or protein complexes e.g. enzymes, members of the immunoglobulin superfamily, hormones, DNA-binding proteins. The linker provides fusion proteins which have greater stability and are less
                                                                                                                                                                                                                                                                                                                                                                                                                                                     604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFV; multichain protein; immunoglobulin; single chain antibody FV; cancer;
                                                                                                                                                                                                                                                                                                            CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                            CGGCCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                         TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGAACAGTAAGAACACCCTATACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAAATGAACTCTCTGAGAGCCGAGGACACACGCGTGTATTACTGTGCAAGACATAACT 301
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                 365 aagtgaagcttgtggagtctgggggaggcttagtgaagcctggagggtccctgaaactct 424
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                                                                                                                                                                                                                                                     2 AGGIGCAGCIGGAGICIGGGGGGGGGGGTGIGCAGCCTGGAAGGICCCIGAGACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "sequence coding for peptide linker 218"
376..708
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                                                                                                                                                                                              73.3%; Score 257.4; DB 21; Length 721; 83.9%; Pred. No. 1.6e-70;
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'note= "sequence coding for A33 Vl region"
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                                                                                                                                                                                                                           56; Indels
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                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCFV
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1..711
/*tag= a
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Example; Fig 12; 42pp; English.
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                                                                                                                        susceptible to aggregation.
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Matches 291; Conservative
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1..321
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                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding fusion polypeptide including protease resistant linker - for making single-chain Fv antibody fragments, e.g for diagnosis and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
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Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                            Whitlow MD;
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                                                                                                            07-APR-1994;
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US5856456-A.
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677 tagtcccgtttgcttactggggccaagggactctggtcactgtctct 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a linked fusion protein containing the amino acid linker of the invention. The linkers are used for connecting constituent polypeptides to form novel linked fusion polypeptides. Polypeptides derived from any protein can be connected, in particular multichain protein or protein complexes e.g. enzymes, members of the immunoglobulin superfamily, hormones, DNA-binding proteins. The linker provides fusion proteins which have greater stability and are less
                                                                                                                                                                                                                Fusion protein; linker; linked fusion polypeptide; multichain protein; protein complex; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide linkers, linked fusion polypeptides containing the linkers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;
                                                                                                                                                                    Linked fusion protein A33/218 sFv coding sequence.
  BP
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92US-0980529.
93US-0002845.
AAZ37398 standard; DNA; 733
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Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Filpula DR, Whitlow MD;
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P-PSDB; AAY54837.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-1994;
20-NOV-1992;
15-JAN-1993;
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                                                                                                            08-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                   US5990275-A
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                                                                                                                                                                                                                                                                                                           Synthetic.
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Search completed: October 11, 2001, 15:12:35
Job time: 6467 sec
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1, Appli 14, Appl 21, Appl

Sequence Sequence Sequence Sequence

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APPLICANT: Hollander, Trwin
APPLICANT: Hollander, Syan
APPLICANT: Holloomb, Ryan
APPLICANT: Holloomb, Ryan
APPLICANT: Tsou, Hwel-Ru
APPLICANT: Weiss, Martin J,
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Apperts and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: May Jersey
COUNTRY: U.S.A.
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IIBM FC COMPATIBLE
OFERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BATNHARG Elizabeth M.
REGISTRATION NUMBER: 31,088
FROM NUMBER: 31,088
US-08-331-398A-59
US-08-31-397B-59
US-08-759-804A-51
US-08-731-397B-31
US-08-759-804A-31
PCT-US-08-759-804A-31
US-08-487-761-14
US-08-398-612A-21
US-08-398-612A-21
US-08-398-612A-21
US-08-398-612A-21
US-08-398-612A-21
US-08-398-613A-21
US-08-491-334A-21
US-08-491-334A-21
US-08-491-334A-21
US-08-491-334A-21
US-08-491-334A-21
US-08-491-334A-21
US-09-027-449-18
US-09-027-985-18
US-09-038-985-18
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One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-08-253-877C-56
Sequence 56, Application US/08253877C;
Patent No. 5773001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T: Hamann, Philip R.
T: Hinman, Lois
T: Hollander, Irwin
T: Holcomb, Ryan
T: Hallett, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 413 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6..413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hamann,
        ; NAME/KEY: CDS
; LOCATION: 6..4
US-08-253-877C-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56, 1
Sequence 56, 1
Sequence 15, 1
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Sequence 17,
Sequence 19,
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                                                                                                                                                                                     Search time 87.94 Seconds
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1 CAGGTGCAGCTGGTGGAGTC......CTACAGTGACTGTTTCTAGT
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-452-164A-56

US-08-926-789-15

US-08-926-789-17

US-08-926-789-17

US-08-926-13152-3

US-08-926-13152-3

US-08-926-13152-3

US-08-926-176A-3

US-08-672-176A-5

US-08-672-176A-5

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US-08-672-176A-5

US-08-672-176A-5

US-08-68-119-15

US-08-483-199-15

US-08-483-199-15

US-08-484-508-15

US-08-853-497A-17

US-08-853-497A-17

US-08-853-497A-17

US-08-853-497A-17

US-08-813-98-82

US-08-813-98-82

US-08-813-98-82

US-08-813-98-82

US-08-813-98-82

US-08-813-98-82

US-08-750-840A-21

US-08-750-840A-21

US-08-750-804-82

US-08-750-804-82

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US-08-750-804-82

US-08-750-804-82

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US-08-750-804-82
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                     October 11,
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Match 1
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Maximum DB :
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TOPOLOGY: linear
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                                                                               US-08-452-164A-56
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US-08-224-591-15
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COUNTRY:
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Sequence 56, Application US/08452164A

Patent No. 5877206.

GENERAL INFORMATION.

APPLICANT: Haman, Philip R.

APPLICANT: Hollander, Italian

APPLICANT: Weiss, Martin J.

ITILE OF INVENTION: Conjugates of Methyltrithio Antitumor

ITILE OF INVENTION: Agents and Intermediates for Their Synthesis

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Home Products Corporation

STREET: One Campus Drive

CITY: Parsippany

CONTRY: New Jersey

CONTRY: U.S.A.
                                                                                                  62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
                                                                                                                                                                               124 CCTGTGCAGCCTCTGGATTCGCTTTCAGTACCTATGACATGTCTTGGGTTCGCCAGACTC 183
                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                   242 IGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT, 301
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                61
                                                                               2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                  CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTATT
                                                                                                                                                                                                                                                                                 TAGACACTGTGCAGGGCCGATTCACCATCTCCCAGAGACATAGTAAGAACACCCTATACC
                                              ö
             Length 413;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  302 ACGCCAGTTTTGCTTACTGGGCCCAAGGGACTACAGTGACTGTTTCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/452,164A FILING DATE: 26 MAY-1995
               DB 1;
             Score 257.4; DB Pred. No. 3.7e-77.0; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,368-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLLIN CALL.

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201,683-2158
            73.3%;
83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: (LENGTH: 413 base pairs TYPE: nucleic acid
                                              Matches 291; Conservative
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             Query Match
Best Local Similarity
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Patent No. 5856456
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   Indels
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Pred. No. 3.7e-77;
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APPLICATION NUMBER:
IS-JAN-1993
APPLICATION NUMBER:
IS-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME:
Goldstein, Jorge A.
REGISTRATION NUMBER:
29,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,591
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                         73.3%;
83.9%;
                                                                                                                                                      Query Match 73.3
Best Local Similarity 83.9
Matches 291; Conservative
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MOLECULE TYPE: CDNA FEATURE:
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                                        NAME/KEY: CDS
LOCATION: 6..4
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242 TGCAAATGAACTCTCTGAGAGCCGAGGACACACGCGTGTATTACTGTGCAAGACATAACT 301
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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                                                         NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/224,591
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APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker I
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler
    APPLICATION NUMBER: US 07
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                            CDS
join(1..711)
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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; LOCATION;
US-08-926-789-15
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US-08-224-591-17
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Patent No. 5990275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                       56; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
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Pred. No. 4.8e-77;
0; Mismatches 56
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FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                   INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LEWTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                               73.3%;
83.9%;
  (202) 371-2540
                                                                                                                                                                                                                                                               Query Match 73.3:
Best Local Similarity 83.9:
Matches 291; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: joir
US-08-224-591-15
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TELEFAX:
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SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
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Matches 291; Conservative
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                                                                                  FILING DATE
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US-08-926-789-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 257.4; DB 2; Length
Pred. No. 4.8e-77;
0; Mismatches 56; Indels
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APPLICANT: Whitlow, Marc
APPLICANT: Whitlow, Marc
TITLE OF INVENTION: Linker For Linked Fusion Pol.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREST: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
SID: 20005
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/002,845

FILING DATE: 15-JAN.1993

APPLICATION NUMBER: US 07/980,529

FILING DATE: 20-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: GOLGStell, JORGE A.

REGISTRATION NUMBER: 29,021

REGISTRATION NUMBER: 0977.1920002/JAG

TELEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2540

INFORMATION FOR SEG ID NO: 17: SEQUENCE CHARACTERISTICS:

LENGTH: 733 base pairs

TYPE: nucleid acid

STRANDEDNES: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08926789 Patent No. 5990275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.3%;
Best Local Similarity 83.9%;
Matches 291; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; LOCATION:
US-08-224-591-17
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62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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Sequence 19, Application US/08579378A
Sequence 19, Application US/08579378A
Sequence 19, Application US/08579378A
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive With
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/926.789
                                                                                                       CLEASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/224,591
FILING DATE: 18-Jan-1993
FILING DATE: 15-Jan-1993
FILING DATE: 15-Jan-1993
FRIOR APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 09/71.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPRAK: (202) 371-2240
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 257.4; DB 3
Pred. No. 4.8e-77, 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%;
83.9%;
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APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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              356 ACGGGTATTTTGACTACTGGGGCCCAAGGCACCCTGGTCACAGTCTC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOER 1059-PCT-PFF/NDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.3%; Score 246.8; DB 5
84.1%; Pred. No. 2.3e-73;
iive 0; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY AGENT INFORMATION:
NAME: NORMEN D. HANSON
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFRAS: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                             ADDRESSEE: Felfe Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                              PCT-0S96-13152-3; Sequence 3, Application PC/TUS9613152; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1329 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 84.19
Matches 291; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1,,1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
PCT-US96-13152-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ADDRESSEE: Townsend and Townsend and Crew STREET: One MarketPlaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 246.8; DB 4;
Pred. No. 1.3e-73;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-ANG-1995
PRIOR APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-ANG-1995
FILING DATE: 19-SEP-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Liebescheutz, JOG O. REGISTRATION NUMBER: 37,505 REFERENCE/DOCKET NUMBER: 118 TELECOMMUNICATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.3%;
Best Local Similarity 84.1%;
Matches 291; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..405
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                                                                           STATE: C
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239 AAGACACTGTGACGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACC 298
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                                                                                                                                                                                              299 TGGAAATGAGCAGTCTGAGGACACGGCCATGTATTACTGTGCAAGGGAGGACT
                                                                                                                                                                        242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT
                                                                           182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
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                                                                                                                                                                                                                                                                     302 ACGG------CAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTCT 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

APPLICANT: do Couto Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides With Broad

TITLE OF INVENTION: Carcinoma Specificity, and Kit and

TITLE OF INVENTION: Diagnostic Vaccination and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SECUENCES: 96

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: V. AMZEL & ASSOC.
STREFT: 2055 No. 5804187th Broadway, Suite 201
STATE: Walnut Creek
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-73;
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Pred. No. 6.3e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CRFCC-008A
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-129-930B-27; Sequence 27, Application US/08129930B; Patent No. 5804187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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ilarity 82.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 418 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Matches 295; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.

APPLICANT: decriani Dr., Roberto L.

APPLICANT: Peterson Dr., Buery A.

APPLICANT: Padlan Dr., Eduardo A.

APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity

TITLE OF INVENTION: and Therapeutic Methods.

NUMBER OF SEQUENCES: 81

CORRESONDENCE ADDRESS:
                                                                                               242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
                                                                                                                        59 AAGTGCAGATGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 CCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGCCATGTCTTGGGTTCGCCAGTCTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACATAGTAAGAACACCCTATACC
                           119 CAGACAGTGTGAAGGGCCGATTCACCATCTCCAGAGATAATGCCAAGAACACCCTGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGGIGCAGCIGGIGGAGTCIGGGGGAGGCGITGIGCAGCCIGGAAGGICCCIGAGACTCI
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                                                                                                                                                                                         302 ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTC 347
                                                                                                                                                                                                                          299 ACGGGTATTTTGACTACTGGGCCAAGGCACCCTGGTCACAGTCTC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 244.8; DB 1;
Pred. No. 6.3e-73;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: PRETTY, SCHROEDER & POPLAWSKI
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P66 38227
                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/07977696C
Patent No. 5792852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION: (510) 748-6868
TELEFAX: (510) 748-6688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 69.7%;
Best Local Similarity 82.9%;
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 418 Dass palrs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PRETTY,
STREET: 444 South F
CITY: Los Angeles
STATE: California
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119 CCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGCCATGTCTTGGGTTCGCCAGTCTC 178
                                                                      182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC 241
                                                                                                                                                                                               242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
                                                                                                                                                                                                                                                                  302 ACGG------CAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT 348
                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08672176A
Patent No. 5908925
GENERAL INFORMATION:
APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
TITLE OF INVENTION: Specificity for Glycated Albumin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: humanized A717 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Silver, Robert S.
REGISTRATION NUMBER: unknown
REGISTRATION NUMBER: u1042/20002
TELECHONE: 215-567-2010
TELEPHONE: 215-751-1142
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs/120 amino acid residues
TYPE: nucleic acid/amino acid residues
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTAL 19104

COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage

AMDIUM TYPE: nos 4.0 or better
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Exocell, Inc.
STREET: 3508 Market Street, suite 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS 4.0 or better SOFTWARE: Wordperfect, Version 5.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,176A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: unknown
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: N/A
INDIVIDUAL ISOLATE: N/A
STRAGE: N/A
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CITY: Philadelphia
STATE: Pennsylvania
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TISSUE TYPE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AGGTGCAGCTGGAGTCTGGGGAGGCCTAGTGCCTGGAGGGTCCCTGAGACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TGCAAATGAACTCTCTGAGAGCCGAGGACACCGCGTGTATTACTGTGCAAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Colon, Margo P.; Shearman, Clyde W.
TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
TITLE OF INVENTION: Specificity for Glycated Albumin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Excell, Inc.
STREET: 3508 Market Street, suite 420
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                      MAP POSITION:
UNITS:
FEATURE: human framework regions; murine CDRs
NAME/KEY: FR-1; CDR-1; FR-2; CDR-2; FR-3; CDR-3; FR-4
LOCATION: aa#1-30; aa#31-35; aa#36-49; aa#50-66;
LOCATION: aa#67-98; aa#99-109; aa#110-120
IDENTIFICATION METHOD: similarity to known sequences
OTHER INFORMATION: antigen is human glycated albumin AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.5%; Score 240.6; DB 2;
82.3%; Pred. No. 1.5e-71;
tive 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08672176A Patent No. 5908925 GENERAL INFORMATION:
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: plasmid
LIBRARY: N/A
CLONE: pluATIVH-1
CLONE: pluATIVH-1
CLONE: PLUATIVH-1
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.5
Best Local Similarity 82.3
Matches 292; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT
FILING DA
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                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                 VOLUME:
ISSUE:
PAGES:
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122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTAT 181
                                                                                                                                                                                                                                                                                             182 CAGACAGTGTGAAGGGCCGATTCACCATCTCCAGAGAACAATTCGAAGAACACGTTGTACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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                           2 AGGTGCAGCTGGTGGAGTCTGGGGGGGGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61
                                                            2 AGGTGCAGCTGGTGGAGTCTGGGGGGAGGCCTAGTGCAGCCTGGAGGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                               182 TAGACACTGTGCAGGCCCGATTCACCATCTCCCAGAGACAATAGTAAGAACACCCTATACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 -- CATAACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTC 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: CHIRON CORPORATION INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/475,000
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 239.8; DB 1;
Pred. No. 2.8e-71;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08475000 Patent No. 5811267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.3%;
ilarity 82.2%;
Conservative (
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NAME: SAVEREIDE, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 357 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: INTELLECT
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Best Local Similarity
Matches 290; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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; LOCATION:
US-08-475-000-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-08-475-000-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEAUTE: HuA717VH-1 linked to HuA717VL
NAME/KEY: HuA717VH; linker; HuA717VL
LOCATION: aa# 1-120; aa# 1-121; aa# 134-240
LOCATION: AA# H-120; aa# 131-133; aa# 134-240
LOCATION: AA# H-120; aa# 131-133; aa# 134-240
LOCATION: AA# H-120; aa# H-120;
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: dlskette, 3.50 inch, 1.4 Mb storage
COMPUTER: PC
                                                                                                                                                             OPERATING SYSTEM: DOS 4.0 or better SOFTWARE: Wordperfect, Version 5.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,176A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTREACH
ANTI-SENSE: no-
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

PUBLICATION DATE:

RELEVAT RESIDUES IN SEQ ID NO:
US-08-672-176A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE: plasmid
LIBRARY: N/A
CLONE: pHuA/17ScFv-1
POSITION IN GENOME: N/A
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: N/A CELL TYPE: N/A CELL LINE: N/A ORGANELLE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 292; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: yes
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                                                                                                                                        COMPUTER:
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JOURNAL:
                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME:
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                          2 AGGTGAAGGTTGTGGAGTCTGGGGGAGTCTTAGTGAGGCCTGGAGGGTCCTGAAACTCT
                                                                                                                                                                                                                                                           182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCTATACC
                                                                                                                                                                                                                                                                                  182 CAGACAGTGTGAAGGGTCGATTCACCGTCTCCAGAGACAATGCCATGAGCAGCTGTACC
  2 AGGTGCAGCTGGAGGTCTGGGGGGGGGGGTGCTGCAGGCTCCCTGAGACTCTCT
                                                                                                                                                                                                                                                                                                                                              242 TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCGGTGTATTACTGTGCAAGACA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,508
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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Pred. No. 2.8e-71;
0; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08484508 Patent No. 5948647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.3%;
82.2%;
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NAME: SAVEREIDE, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.3
Best Local Similarity 82.2
Matches 290; Conservative
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OPERATING SYSTEM:
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US-08-484-508-15
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                                                                                                                                                                                                                                                                             182 CAGACAGTGTGAAGGGTCGATTCACCGTCTCCAGAGACAATGCCATGAGCAGCCTGTACC 241
                                                                                                                                                                                                                                                                                                                                                                     62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
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2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61
                          2 AGGTGAAGGTTGTGGGAGGTCTGGGGGGAGTCTTAGTGAGGCCTGGAGGTCCCTGAAACTCT 61
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Sequence 15, Application US/08483199
Sequence 15, Application US/08483199
Sequence 15, Application US/08483199
Setent No. 5849877
SERENAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIGONY
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
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Pred. No. 2.8e-71;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,199
FILING DATE: 07-40N-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0850.009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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TELEPAX: (510) 655-3542
INPORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.3%;
82.2%;
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Best Local Similarity 82.2
Matches 290; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94662-8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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; LOCATION:
US-08-483-199-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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296
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                   61
182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACATAGTAAGAACACCCTATACC
                                                                                                                                                TGCAAATGAACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACA----
                                                                                                                                                                                  297 -TAACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTGACTGTTTCT 348
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Search completed: October 11, 2001, 15:14:12 Job time: 4999 sec

us-08-791-391a-2.rpr

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; Search time 31.63 Seconds
(without alignments)
281.771 Million cell updates/sec
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1 QVQLVESGGGVVQPGRSLRL.....RHNYGSFAYWGQGTTVTVS 117
                    Compugen Ltd.
                                                                                                                                                                                                                                                                                                           219241 seqs, 76174552 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                                                           October 11, 2001, 11:57:35

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                               Title:
Perfect score:
Sequence:
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                                                                         OM protein
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summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_68:* Database

1: pirl:* 2: pir2:* 3: pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

chain - l chain V chain chain V chain V chain V chain Description heavy SUMMARIES \$31108 \$331107 \$19666 \$38489 \$31588 \$31588 \$31686 \$31686 S31603 S31117 S48797 G36005 D36005 \$31666 \$48798 \$46392 S78486 S05271 A49028 S23624 155673 S31701 S46390 S31699 Query Match Length DB 881.7 881.5 881.5 881.5 881.5 880.0 880.0 880.0 779.0 Score 493.5 492.5 492 492 491.5 490 488.5 487 485.5 485.5 485 507 503 503 503 503 503 503 502 502 500 500 509 6498 798 Result õ

Ig heavy chain V r	Ig heavy chain V r			Ig heavy chain V r	heavŷ	varia	Ig heavy chain - h	heavy	heavy	heavy	heavy chain				
S20782	S31674	S36278	S30531	S31598	S31120	137780	S31112	M3HUAM	PH1649	538493	S31601	PH1648	PL0098	PH1647	826794
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124 2	139 2	120 2	125 2	135 2	114 2		120 2	122 1	109 2					112 2	123 2
						147	-			123	130	108	130		
78.7	78.7	78.6	78.6	78.6	78.3	78.3 147	120	78.2	78.1	77.9 123	77.9 130	77.8 108	77.4 130	77.4	77.3

ALIGNMENTS

RESULT S31108

219241

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

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Igheavy chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Date: O2-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur, J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A;Reference number: S31104; MUID:92111633
A;Accession: S31108
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Residues: 1-119 <RAA>
A;Residues: 1-119 <RAA>
A;Rosserreferences: EMBL;X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (30pl) - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996 C; Accession: C36005 R; Schroeder Jr., H.W.; Wang, J.Y. Proc. Natl. Acad. Sci. U.S. A. 87, 6146-6150, 1990 A; Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge A; Accession: C36005 WuID: 90349571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.3%; Score 507; DB 2; Length 119;
82.4%; Pred. No. 2e-39;
ive 8; Mismatches 11; Indels
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A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
A; Cross-references: GB:M18513
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 82.4%;
Matches 98; Conservative
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Best Loc Matches

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Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Decies: Homo saplens
C;Decession: 538489
S;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe submitted to the EMBL Data Library, June 1993
A;Decession: Human antibody fragments specific for human blood group antigens from A;Accession: 538489
A;Accession: 538489
A;Accession: by A;Accession: 538489
A;Accession: 538
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C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S31588
R; Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate 1A; Reference number: S31588
A; Accession: S31588
                                                                                       A;Cross-references: EMBL:Z23028; NID:g414025; PIDN:CAA80563.1; PID:g414026 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer: immunoglobulin homology <IMO. F;15-98/Domain: immunoglobulin homology <IMO.
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12;
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7
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80.2%; Pred. No. 5.4e-39;
ive 11; Mismatches 9;
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Pred. No. 4.8e-39;
6; Mismatches 11;
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Ig heavy chain V region - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.7%;
Best Local Similarity 77.2%;
Matches 98; Conservative 6
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Best Local Similarity
Matches 97; Conserv
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A; Residues: 1-140 <CUI>
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C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C; Accession: 51966
R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A; Title: By-Passing immunization. Human antibodies from V-gene libraries displayed on pi A; Reference number: 519666
A; Accession: 519666
A; Coss-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C; Superfamilly: Immunoglobulin V region; Immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology cimel Fis-98/Domain: immunoglobulin homology cimel
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                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                           10; Indels
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                                                             Score 503; DB 2;
Pred. No. 4.5e-39;
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Pred. No. 4.6e-39;
6; Mismatches 13
                                                                                                                           9; Mismatches
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81.0%;
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82.4%;
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Best Local Similarity 81.0°
Matches 98; Conservative
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Best Local Similarity
Matches 98; Conserv
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Ig heavy chain V region (M72) - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C; Accession: E36005
R; Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S. A. 87, 6146-6150, 1990
A; Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge A; Accession: E36005
A; Accession: E36005
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C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
R;Culsinier, A.M.; Guthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Reference number: S31585
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                                                    20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWYRQAPGKGLEWVAVISYDGSNKYY 79
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                             QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
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                                                                                                                            61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY
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Pred. No. 1.2e-38;
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Pred. No. 7.8e-39;
5; Mismatches 13
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A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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81.1%;
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82.1%;
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Ig heavy chain V region - human
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Best Local Similarity 81.17
Matches 99; Conservative
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A; Cross-references: GB:M34030
C; Genetics:
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A Molecule type: mRNA
A Residues: 1-132 <CUI>
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Best Local Similarity
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| SS 122
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C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S31686
S; Gauthier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31585
A; Accession: S31686
A; Status: preliminary
A; Molecule type: mRNA
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: Sil679
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: Sil585
A;Accession: Sil679
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                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin P;34-117/Domain: immunoglobulin homology <IMM>
1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY
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Pred. No. 7.8e-39;
5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 140;
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Pred. No. 6.6e-39;
9; Mismatches 11;
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Ig heavy chain V region - human (fragment)
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80.2%;
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83.8%;
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Best Local Similarity 80.23
Matches 97; Conservative
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A; Residues: 1-134 <CUI>
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us-08-791-391a-2.rpr

F;15-98/Domain: immunoglobulin homology <IMM>

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Gaps

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Indels

15;

Mismatches

9

Conservative

96;

Matches

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R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge A;Feference number: A36005; MUID:90349571
A;Accession: D36005
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R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable A;Reference number: A36005; MUID:90349571
A;Accession: G36005
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D36005
Ig heavy chain V region (M43) - human
Ig heavy chain V regions (Man)
C;Species: Homo sapiens (man)
C;Dete: 21.Dec.1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: D36005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Homo sapiens (man)
C.Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
                                                                                                                                                                                                                                                                                                     61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNY-----GSFAY-----WGQ 109
                                                                                                                                                                                                                                                                                                                                       61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARH----NYGSFAYWGQGTTVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                    Indels
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Pred. No. 1.3e-38;
                                  Score 498.5; DB 2
Pred. No. 1.3e-38;
                                                                                                    5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (M74) - human
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81.0%;
                                  80.9%;
78.1%;
                                                                                                    Conservative
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Best Local Similarity
Matches 98; Conserv
                                     Query Match
Best Local Similarity
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A; Residues: 1-121 <SC
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                                                                                                    Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 02-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C; Accession: S31117
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A; Reference number: S31104; MUID:92111633
A; Reference number: S31117
A; Accession: S31117
A; Accession: S31117
A; Accession: S31117
A; Accession: S1117
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A; Accession: Acces
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A;Residues: 1-128 < CMAH>
A;Cross-references: BMBL:246379; NID:9587147; PIDN:CAA86512.1; PID:91340168
A;Cross-references: EMBL:246379; NID:9587147; PIDN:CAA86512.1; PID:91340168
B;Tomlinson, I.M.; Malter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: $26885; MUID:93021117
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
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9
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-98 COMA
A; Crosa-references: EMBL: $212350; NID: 932922; PIDN: CAA78220.1; PID: 932923
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                              1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY
                                                                                                                            LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS
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Pred. No. 1.2e-38;
5; Mismatches 14
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Best Local Similarity 80.3%;
Matches 98; Conservative
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A; Residues: 1-122 <RAA>
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| SS 122
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Ig heavy chain V region (M49) - human C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 3.1-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: F36005
R:Schroeder Jr., H.W.; Wang, J.Y.
R:Schroeder Jr., H.W.; Wang, J.Y.
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A:Reference number: A36005; MUID:90349571
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                                                                     A;Generi GDB:IGH0; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33
A;Map position: 14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
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Matches 98; Conservative
                            A;Cross-references: GB:M34024
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A; Residues: 1-119 <SCH>
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A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
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X MEDLINE=81013859; PubMed=6774332;

X MEDLINE=81013859; PubMed=6774332;

X Lebman D.W., Putnam F.W.;

T anino acid sequence of the variable region of a human mu chain:

I location of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

C -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH MACROGLOBULINEMIA.

PATIENT WITH MACROGLOBULINEMIA.

R HSSP; P01772, 2162.

R HSSP; P01772, 2162.

R InterPro: IPRO3006; -.

R Pfam: PF00047; 1g; 1.
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AC P01771;
DT 21-JUL-11986 (Rel. 01, Created)
DT 21-JUL-11986 (Rel. 01, Last sequence update)
DT 15-JUL-11999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
DF IG HEAVY CHAIN V-III REGION HIL.
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HV28_MOUSE
HV17_MOUSE
HV19_MOUSE
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HV33_MOUSE
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HV41_MOUSE
HV3P_HUMAN
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HV32_MOUSE
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HV3H_HUMAN
HV55_MOUSE
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HV3C_HUMAN
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HV02_CANFA
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    protein search, using sw model

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HV16_MOUSE
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HV16_MOUSE
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dreker L., Schwarz J., Reichel W., Hilschmann N.; Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the characterization of the protein, the L- and H-chains, the Grangen Promide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG H11.";
Biochemistry 18:553-560(1979).
-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ponsting1 H., Hilschmann N.; The primary structure of a "The rule of antibody structure. The primary structure of a
                                                                                                                                                                                                                                                                        Score 456, DB 1; Length 121;
Pred. No. 3.6e-39;
9; Mismatches 19; Indels
                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
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121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                     MEDLINE=79124695; PubMed=420800;
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Best Local Similarity 73.6%;
Matches 89; Conservative
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InterPro; IPR003006; -
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
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 Homo sapiens (Human)
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                                    NCBI_TaxID-9606;
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P01770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-81234548; Pubmed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
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                                                                                                                                                                                                                                                      Score 453; DB 1; Length 119;
Pred. No. 7e-39;
                                                                                                          PYRROLIDONE CARBOXYLIC ACID.
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13242 MW; C96935A6E55E165B CRC64;
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DN -> ND (IN REF. 2).

W -> H (IN REF. 2).

Y -> W (IN REF. 2).
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MEDLINE=77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
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InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region; Signal.
NON_TER 1 1 1
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1 Similarity 75.6%;
90; Conservative
HSSP; P01772; 21G2.
InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
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96
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119 AA;
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Best Local Similarity
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                                                                         18 VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHYA 77
                                                                                               62 DIVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-HNYGSFA--YWGQGTTVTVSS 117
                                                                                                       78 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPYYAMDYWGQGTSVTVSS 136
                                                                                                                                                                                                                                                                                                                   Marquart M., Delsenhofer J., Huber R., Palm W.; Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment at 3.0
                                                                                                                                                                                                                                            SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgGl KOL, I.";
Poppe-Seyler's Z. Physiol. Chem. 364;713-747(1983).
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                 3;
                                Score 451.5; DB 1; Length 136; Pred. No. 1.1e-38;
                                                 Indels
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        136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
                                                  15;
                        73.3%; SCO1.

7 74.8%; Pred. No. 1.1.

've 12; Mismatches
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                                                                                                                                                       126 AA
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MEDLINE-81072295; Pubmed=7441755;
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PDB; 2IG2; 12-JUL-89.
InterPro: IPR003006; -
Pfam; PF00047; ig; 1.
Immunoglobulin V region; 3D-structure.
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IG HEAVY CHAIN V-III REGION KOL.
                                                                                                                                                                                                                                                                                                                                             and 1.0-A resolution.";
J. Mol. Biol. 141:369-391(1980).
PIR; A02055; GIHUKL.
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                89; Conservative
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                                        Local Similarity
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MEDLINE-81101090; PubMed-6450418;
Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region."
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
                                                                                                                                                                                                                              1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVROAPGKGLEWVAKVSSGGGSTYY
                                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                            Length 126;
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85.7%; Pred. No. 3.5e-38;
ive 8; Mismatches 6; Indels
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124
126
13718 MW; E4D71B52B16F8776 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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Best Local Similarity 85.7
Matches 84; Conservative
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117 AA;
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126 AA;
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PRT;
                                           Interpro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
SEQUENCE 116 AA: 12730 MW;
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71.88;
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HSSP; P01772; 21G2.
InterPro; IPR003006; -.
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                PIR; A02064; M3HUGL.
HSSP; P01772; 2IG2.
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Best Local Similarity
MACROGLOBULIN.
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SEQUENCE
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HV55_MOUSE
ID HV55_MC
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HV3H_HUMAN
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Goni F., Frangione B.;

Goni F., Erangione B.;

Famino acid sequence of the Fv region of a human monoclonal IgM

(protein WEA) with antibody activity against 3,4-pyruvylated

galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acid. Sci. U.S.A. 80:4837-4841(1983).

-I MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

AGAINST 3,4-PYRUYYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH

WALDENSTROM'S MACROGLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mutype), subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilschmann N.;
Submitted (JUN-1975) to the PIR data bank.
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION WEA.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V-III REGION GAL.
                                                                  114 AA.
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REVISION TO THE COMPOSITION OF 28-33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
Immunoglobulin V region.
                                                              STANDARD;
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HSSP; P01772; 21G2.
InterPro; IPR003006;
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P01781;
                                                              HV3B_HUMAN
P01763;
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MEDLINE=74175307; Pubmed=4208843;
Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
Blochemistry 13:2482-2488(1974).
-i - MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
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                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION GA.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                Length 116;
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2C67CA9AAAA1282 CRC64;
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                                                         Score 441.5; DB 1;
Pred. No. 9.7e-38;
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us-08-791-391a-2.rsp

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Gaps

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Length 115;

P18526;

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MEDLINE-79151016; PubMed=107164;
Putnam F.W. Liu Y.-S.W., Low T.L.K.;
Putnam F.W. Liu Y.-S.W., Low T.L.K.;
Primary Structure of a human ighl immunoglobulin. IV. Streptococcal Ighl protease, digestion, Fab and Fc fragments, and the complete amino acid sequence of the alpha 1 heavy chain.";
J. Biol. Chem. 254:2865-2874(1979).
PIR; A02056; AlHUBR.
HSSP; POIT72, 2163.
InterPro; IPR003006; --
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Glycoprotein.
                                                                                                                          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                               1 QVQLVESGGGVVQAGTSLRLSCTASAFNLSDYAMHWYRQAPGKGLZWVALISYGGSBTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carassius auratus (Goldfish).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.
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1-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16-HEAVY CHAIN V-III REGION BUR.
16 HEAVY CHAIN V-III REGION EUR.
EURATYOLA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidee; Homo.
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                                                                                        14; Indels
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12379 MW; 208876A7DF52DCF4 CRC64;
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                                                   68.8%; Score 424; DB 1;
69.2%; Pred. No. 5.5e-36;
iive 20; Mismatches 14,
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 5A PRECURSOR.
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                                                                                      81; Conservative
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119 1
119 AA;
115 AA;
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Best Local Similarity
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P01773;
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P19181;
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HV3L_HUMAN
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Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain of a human igaz immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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; Pred. No. 2.2e-36;
11; Mismatches 7; Indels
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
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COMPLEMENTARITY-DETERMINING
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           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 345 PRECURSOR.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 HEAVY CHAIN V-III REGION BUT.
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InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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81.6%;
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
                                                                                        Mus musculus (Mouse)
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                         NCBI_TaxID=10090;
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P01767;
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                              MEDLINE-88144476; PubMed-3125551; Walson M.R., Middleton D., Warr G.W.; "Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/CJ;
MEDLINE-89279149; PubMed-2499654;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
I. HIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
PIR; JT0505; HW884.
Interpro; IPR003006; -.
PFam; PF00047; 19; 1.
                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                        Length 116;
                                                                                                                                                                       COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
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                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                         9C2279E2DF199B12 CRC64;
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                                                                                                                                                                                                                                                                        DB 1;
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8
                                                                                    Sci. U.S.A. 85:1566-1570(1988)
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01-NOV-1990 (Rel. 16, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
16 HEAVY CHAIN V REGION 5-84 PRECURSOR.
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BY SIMILARITY
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FRAMEWORK 1.
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SIGNAL 1 19 19 IG
                                                                                                                               Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                          12808 MW;
                                                                                   Proc. Natl. Acad. Sci. U
PIR; B28966; B28966.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                      SEQUENCE FROM N.A.
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NCBI_TaxID=7957;
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ID HV54_MOUSE
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SEQUENCE
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
THAT BINDS GALACTAN.
                                                                  Gaps
                                                                                                                        1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                   20 EVKLVESGGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVAYISNGGGSTYY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-79223895; PubMed-111245; Rao D.N., Rudikoff S., Krutzsch H., Potter M.; Rao D.N., Rudikoff S., Krutzsch H., Potter M.; Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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         Length 117;
                                                               8; Indels
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      67.9%; Score 418; DB 1;
79.6%; Pred. No. 2.2e-35;
ive 12; Mismatches 8
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HV37_MOUSE
TD HV47_MOUSE STANDARD; PRT; 119 AA.
RO P01807;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 12-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                        61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
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Query Match
Best Local Similarity 79.69
Matches 78; Conservative
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Best Local Similarity 65.3
Matches 77; Conservative
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InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
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HSSP; P01810; 2FBJ.
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01-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-:- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.4%; Score 483; DB 4; Length 116; Best Local Similarity 81.0%; Pred. No. 2e-43; Matches 94; Conservative 5; Mismatches 17; Indels
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12434 MW; 0DA0348154DD6061 CRC64;
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InterPro; IPR003006; ...
Pfam; PF000047; ig; 1...
SMART; SM00406; IGv; 1...
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SEQUENCE 116 AA; 12434
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  NCBI_TaxID=9606;
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09u172 homo sapten
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Q9u187 homo sapien
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Q9n0w4 oryctolagus
Q9u195 homo sapien
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1 QVQLVESGGGVVQPGRSLRL.....RHNYGSFAYWGQGTTVTVSS 117
                                                                                        Search time 46.3 Seconds
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C., Lichtenstein A.K., Berenson J.R.; A CDIO-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers."; Leukemia 9:1948-1953(1995).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX EMBL; 880866; AAD14339.1; -..
HSSP; P01772; ZFB4.
                                                                                                                                                                                                                                                                                61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR------HNYGSFAYWGQGT 111
                                                                                                                                                                                                               1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.4e-41;
9; Mismatches 18; Indels 9
                                                                                                                                          Length 121;
                                                                                                                                                                            17; Indels
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                                                                                       2F045CCFA5D50736 CRC64;
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Last annotation update)
                                                                                                                                        Score 474; DB 4;
Pred. No. 1:9e-42;
8; Mismatches 17,
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SEQUENCE FROM N.A.
MEDLINE=96071149; PubMed=7475288;
                                                                                       121 AA; 13154 MW;
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76.0%;
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Best Local Similarity 71.4%;
Matches 90; Conservative
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                                                                                                                                                       1 Similarity 76.0 92; Conservative
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SMART; SM00406; IGv; 1.
NON TER 1
   InterPro; IPR003596; -.
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SMART; SM00406; IGV; 1.
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01-MAR-2001
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Best Local S
Matches 92
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998).
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-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGGGGLGLGYWGQGTLVTVSS 116
                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.1%; Score 475; DB 4; Length 113; 79.5%; Pred. No. 1.4e-42; 1ve 6; Mismatches 14; Indels
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01-WAY-2000 (TrEWBLrel: 13, Last seq
01-WAR-2001 (TrEWBLrel. 16, Last ann
                                                                                       PRT;
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HSSP; P01772; 2FB4.
InterPrç; IPR003006; -.
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                                                                                     PRELIMINARY;
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Matches 93; Conser
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                            61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGS-----FAYWGQGTTVTV 115
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion from intermedial phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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112 112
112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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77.0%; Pred. No. 5.7e-41;
tive 11; Mismatches 14;
                                                                                                                                                                                    17;
                                                                                                                                                  DB 4;
                                                                                                                                                74.8%; Score 460.5; DB 73.8%; Pred. No. 5e-41;
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                                                                                           13579 MW;
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Matches 87; Conservative
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Matches 90; Conservative
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InterPro; IPR003596; -. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
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122 1
122 AA;
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                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Saplens (Human).
EUKARYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
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118 Aa; 12872 MW; B4D1A5944B2D5CCA CRC64;
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HSSP; P01772; 2FB4.
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HSSP; P01772; 2FB4.
InterPro; IPR003006;
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InterPro; IPR003596; -.
Pfam; PF00047; 19; 1.
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Matches 93; Conserv
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Q9UL84;
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Gaps

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Length 112; Indels

RESULT Q9UL84

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SEQUENCE FROM N.A.

Tange Y., Kayano H.;

"Human VH gene sequence.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                              --ARHNYGSFAY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYYL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VQLEESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bustrycha: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 414; DB 4; Length 95;
Pred, No. 2.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 95 95 90A8C6D16D22574A CRC64;
                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
IMUNOSLOBULIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
              59 YYLDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC-
                                                                                                                                                                        95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DIVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9QYF0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
CN 8 SCFV.
                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB035268; BAA87067.1; -. HSSP; P01772; 2FB4.
InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.28;
82.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.1:
Matches 78; Conservative
                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                        121 WGQGTLVTVSS 131
                                                                      107 WGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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NON_TER
SEQUENCE
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                                                                                                              Clin. Immunol. Immunopathol. 87:184-192(1998).
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-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                     1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSS--GGGST 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYG-SFAYWGQGTTVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                 Length 118;
                                                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.0%; Score 419; DB 4; Length 131; Best Local Similarity 65.6%; Pred. No. 1.2e-36; Matches 86; Conservative 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                       12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96E7D668E375DEA0 CRC64;
                                                                                                                                                                                                                                                                                              Query Match 74.4%; Score 458.5; DB 4; Best Local Similarity 76.9%; Pred. No. 7.7e-41; Matches 90; Conservative 12; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
                           SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF035026; AAD56262.1; -.
InterPro; IPR003006; -.
InterPro; IPR003396; -.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 AA; 14142 MW;
                                                                                                                                                     EMBL, AF035023, AAD56259.1,
InterPro, IPR003006, -
InterPro, IPR003596; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                      118 AA;
NCBI_TaxID=9606;
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                                                                      foung D.C.;
                                                                                                                                           DOMAIN.
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SEQUENCE
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fetus.";
Clin, Immunol, Immunopathol, 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNY-----GSFAYWGQGTTV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYXCARGLYVVVPAAFSRFDYWGQGTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 124;
                                                                                                                                                                                                                 MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               124 124
124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.1%; Score 382.5; DB 4; Best Local Similarity 58.9%; Pred. No. 7.9e-33; Matches 73; Conservative 19; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AA.
                                  124 AA.
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                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
NON TER 1
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                                PRELIMINARY;
                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=9606;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                      fetus.";
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                                Q9UL92
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Q9UL87
   RESULT
                  Q9UL92
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                STRAIN=BALB/C; TISSUE-SPLEEN;
shinohara N., Demura T., Fukuda H.;
shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wide K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal
antibody (MaD 7, its light and heavy chains) and construction of a
single chain antibody (scPt).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF152372; AAD40243.1; -..
HisSP; PO1842; TFAB.
InterPro; IPR003006; -.
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                             1 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSS-GGIIYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 DIVQGRFIISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                     ;;
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;
                                                                                                                                                                                                                                                  65.5%; Score 403.5; DB 11; Length 298; 64.4%; Pred. No. 1.4e-34; live 20; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 403.5; DB 11; Length 437;
Pred. No. 2.3e-34;
2; Mismatches 20; Indels 3;
                                                                         method.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB03631, 18.
HSSP: P01607; 1REI.
InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam: PF00047; 19; 2.
                                                                                                                                                                                      1406; IGV; 1.
298 AA; 31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 437
437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
GAMMAL HEAYY CHAIN OF MABY (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan; PF00047; 19; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SMART; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                   76; Conservative
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                                                                                                                                                                       Pfam; PF00047; 1g;
SMART; SM00406; IGV
SEQUENCE 298 AA;
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Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 76; Conserv
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A
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NON_TER
SEQUENCE
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InterPro; IPR003006; -

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Gaps

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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zafiropoulos A., Kandilogiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
Krambovitis E.;
"Induction of somatic mutations in human B cells by in vitro
immunization.";
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 59.4%; Score 366; DB 4; Length 112; Best Local Similarity 67.6%; Pred. No. 3.8e-31; Matches 71; Conservative 10; Mismatches 12; Indels 12; Gaps
                                                                                                                                                                                                                  22 CAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYYLDTVQGRFTISRDNSKNTLYL 81
                                                                                                                                                                                                                                      1 CAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                   .;
8
                                                                                                                                              Ouery Match 60.4%; Score 372; DB 4; Length 104. Best Local Similarity 70.2%; Pred. No. 8.1e-32; Matches 73; Conservative 9; Mismatches 14; Indels
InterPro; IPR003600; -.
Pfam; PF00047; 1g; 1.
SMART; SM00410; IG_11ke; 1.
NON_TER 10 1 1
NON_TER 104 A, 11598 MW; 611D1A3F40E96E7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;
                                                                                                                                                                                                                                                                                      82 QMNSLRAEDTAVYYCARHNY---GS-----FAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                        112 AA.
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InterPro; IPR003006; -.
InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SMART; SM00406; IGV; 1.
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Search completed: October 11, 2001, 12:07:34 Job time: 409 sec Н

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Heavy chain variab Human antiFc epsil Human antiFc epsil Murine monoclonal Murine monoclonal Chimeric antibody Human antibody hea
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158.326 Million cell updates/sec
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Vitaxin heavy chai
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Antibody LM609 hea
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                                                                                                       October 11, 2001, 11:45:50 ; Search time 44.8 Seconds
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1 QVQLVESGGGVVQPGRSLRL.....RHNYGSFAYWGQGTTVTVSS
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; anglogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.
                                                                                         Vitaxin antibody heavy chain variable region protein fragment.
                    AAW76001 standard; Protein; 117 AA
                                                                                                                                                                                                                                                         98WO-US01826
                                                                                                                                                                                                                                                                               97US-0791391
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-437472/37.
N-PSDB; AAV49820.
                                                                                                                                                                                                                                                                                                                              Glaser SM, Huse WD;
                                                                                                                                                                                                                                                                                                       (IXSY-) IXSYS INC.
                                                                                                                                                                                                          WO9833919-A2.
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                                           AAW76001;
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RESULT
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Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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                                                                                           This sequence represents a fragment of the vitaxin antibody variable heavy chair region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psorlasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Bahanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of anglogenesis, inflammatory diseases e.g. psoriasis, cancers and
integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                         100.0%; Score 616; DB 19; 100.0%; Pred. No. 2.5e-49;
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                                                                Claim 1; Fig la; 129pp; English.
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                                 angiogenesis or restenosis
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                           117 AA;
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Matches 117;
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Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the LM609 antibody variable heavy chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta and can be used to inhibit binding of alphavbeta1 to a ligand and thus block integrin mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non )immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
fragments can be used in the diagnosis and treatment of alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriaais and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                       Length 117;
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                                                                                                                                                                                                                                       100.0%; Score 616; DB 22; 100.0%; Pred. No. 2.5e-49;
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Best Local Similarity 100.
Matches 117; Conservative
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                                                                                                                                        osteoporosis.
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Mismatches

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Matches 103; Conservative

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etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                   Gaps
                                                                                                                                                             QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                           exhibiting selective binding affinity to alphaybete_3 integrin or their functional fragments. The antibodies or their functional fragments are be used in the diagnosis and treatment of alphaybeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                    present invention relates to enhanced LM609 grafted antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                            alphaVbeta_3 integrin; angiogenesis;
                                                                                                    Score 552; DB 19; Length 117;
Pred. No. 1.7e-43;
Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory; cancer; retina; restenosis; osteoporosis
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                                                                                                     89.6%;
88.0%;
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                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody;
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es 103;
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1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                The present sequence, the heavy chain variable region of the human actiondy (Ab) CRA2, was used in the preparation of a humanised or semi-chimeric monoclonal Ab (MAD), comprising complementarity determining regions (CDR) from a murine, anti-human high affinity immunoglobulin E (IGE) receptor, MAD. The humanised, semi-chimeric or chimeric MAD can be used to treat or prevent diseases, specifically allergies, associated with the receptor, and has very low antigenicity in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region; CDR; murine; mouse; human; high affinity; immunoglobulin E; receptor; monoclonal antibody; IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised, semi-chimeric and chimeric antibodies against human high-affinity IgE receptor - useful medicinally and have low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 539; DB 18; Length 117;
Pred. No. 2.7e-42;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                              chimeric; treatment; prevention; disease; allergy; CRA2
                                                                                                                                                                                                                           Heavy chain variable region of human CRA2 antibody.
                                                                                                                                               Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 13; 26pp; Japanese.
                                                                                                                                          AAW27526 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5%;
86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASAK ) ASAHI BREWERIES LTD.
(NIKKA WHISKEY KK.
(TORI ) TORII YAKUHIN KK.
(TSUK/) TSURA T.
                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0024816
                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0024816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 86.3 nes 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-429186/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                JP09191886-A.
                                                                                                                                                                                                                                                                                                                                                                                                     19-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-1996;
                                                                                                                                                                                                 16-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1997.
                                                                                                                                                                      AAW27526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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                                                                                                                    RESULT
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Length 117;

Score 552; DB 22; Pred. No. 1.7e-43;

89.6%; 88.0%;

Best Local Similarity

Query Match

AAW73874;

9

RESULT

Peptide Protein

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This sequence represents a human antific epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast Pichia pastoris as the host cell. The method can prepare an antibody Fab fragment cost efficiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AntiFc epsilon RI alpha chain antibody; antibody production; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibody; antibody humanisation; antibody engineering; LM609; monoclonal antibody; complementarity determining region; CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                               Preparing an antibody Fab fragment using yeast - in high yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 539; DB 20;
Pred. No. 5.9e-42;
8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine monoclonal antibody LM609 VH region.
                                                                                   /note= "signal peptide"
                                                                                                                 "mature protein"
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 9-10; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06381 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%;
86.3%;
                                                                                                                                                                                                                                                              (ASAK ) ASAHI BREWERIES LTD.
(NIKK-) NIKKA WHISKEY KK.
(TORI ) TORII YAKUHIN KK.
                                                                                                                                                                                                      97JP-0171232
                                                                                                                                                                                                                                 97JP-0171232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 101; Conservative
                                                                                                   23..242
/note= "1
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-124394/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and in high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 AA;
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX01216
                                                                                                                                                                                                                                                                                                         (TSUR/) TSURA I.
                                                                                                                                              JP11000174-A.
                              Homo sapiens
                                                                                                                                                                                                      13-JUN-1997;
                                                                                                                                                                                                                                  13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9929888-A1
                                                                                                                                                                         06-JAN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY06381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                       Peptide
                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a human antific epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast Pichia pastoris as the host cell. The method can prepare an antibody Fab fragment cost efficiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 evqlvesggglvqpggslrlscaasgftfstypmswvrqapgkglewvafisnrggstyy 79
                                                                                                                                                          AntiFc epsilon RI alpha chain antibody; antibody production; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing an antibody Fab fragment using yeast - in high yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 6
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87.5%; Score 539; DB 20;
Best Local Similarity 86.3%; Pred. No. 5.9e-42;
Matches 101; Conservative 8; Mismatches 8;
                                                                                                                               Human antiFc epsilon RI alpha chain antibody #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human antifc epsilon RI alpha chain antibody #4.
                                                                                                                                                                                                                                        /note= "signal peptide"
20..239
/note= "mature protein"
                                                                                                                                                                                                                  Location/Qualifiers
                                       AAW73874 standard; Protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 7; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW73876 standard; Protein; 242
                                                                                                                                                                                                                                                                                                                                                                                                                        BREWERIES LTD.
                                                                                                                                                                                                                                                                                                                                                              97JP-0171232
                                                                                                                                                                                                                                                                                                                                                                                          97JP-0171232
                                                                                                31-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       NIKKA WHISKEY KK.
TORII YAKUHIN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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N-PSDB; AAX01214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and in high yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TSUR/) TSURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                      (ASAK ) ASAHI
                                                                                                                                                                                                                                                                                                     JP11000174-A
                                                                                                                                                                                                                                                                                                                                                             13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-1997;
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31_MAR-1999
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(NIKK-) (TORI)

Sequence

AAW73876;

SEXTXEX

AAW73876

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Gaps

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This sequence represents the light chain V kappa region of murine monoclonal antibody LM609. LM609 is directed to integrin alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides humanised antibodies, especially humanised LM609. In such humanized antibodies, a light chain CDR from a mouse antibody such as LM609 is grafted onto a human light chain, and a heavy chain CDR from a mouse antibody is grafted onto a human antibody heavy chain to produce libraries from which a humanised murine antibody having the desired specificity is selected. By preserving the original CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see AAX06371-72), the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric; antibody; human parathormone related peptide; hPTRP; mouse; L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR; hypophosphaemia; pathogen; vitamin D resistance; V region; C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYYLDT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric antibody against hPTRP H chain V region SEQ ID NO:56.
                                                                                                                                                                                                                                                Production of humanized mouse monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numanisation strategy ensures epitope conservation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.2%; Score 525; DB 20;
86.0%; Pred. No. 5.7e-41;
iive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                        Disclosure; Page 49-50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57591 standard; protein; 118
                                              98WO-US25828.
                                                                                  97US-0986016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-JP03382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0214168
96JP-0255196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.2
Best Local Similarity 86.0
Matches 98; Conservative
                                                                                                                          (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Mus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                  Barbas CF, Rader C;
                                                                                                                                                                                                      WPI; 1999-394979/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130 AA;
                                            04-DEC-1998;
                                                                                  05-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1997;
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26-SEP-1996;
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    17-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57591;
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                                                                                                                                                                                                                                                                                This sequence represents the heavy chain variable region of murine monoclonal antibody LM609. LM609 is directed to integrin alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides humanised antibodies, especially humanised LM609. In such humanized antibodies, a light chain CDR from a mouse antibody such as LM609 is grafted onto a human light chain, and a heavy chain CDR from a mouse antibody is grafted onto a human antibody heavy chain to produce libraries from which a humanised murine antibody having the desired specificity is selected. By preserving the original CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the humanisation strategy ensures epitope conservation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibody; antibody humanisation; antibody engineering; LM609; monoclonal antibody; complementarity determining region; CDR grafting; mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                      Production of humanized mouse monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%; Score 536; DB 20;
85.5%; Pred. No. 5.1e-42;
tive 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "vector-encoded residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine monoclonal antibody LM609 V kappa.
                                                                                                                                                                                                                                              Disclosure; Page 52-53; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06379 standard; Protein; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "CDR2"
96..103
/note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28..32
/note= "CDR1"
                                          97US-0986016
  98WO-US25828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.0°
Best Local Similarity 85.5°
Matches 100; Conservative
                                                                                (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 63
                                                                                                                        Rader C;
                                                                                                                                                              WPI; 1999-394979/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
04-DEC-1998;
                                          05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9929888-A1
                                                                                                                        Barbas CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY06379;
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AAY06379

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Region Region Region

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Gaps

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Length 130; Indels 9

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Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A composition for the treatment of hypercalcenic crisis. active component a substance which inhibits the binding of parathyroid hormone related peptide (PHHP) to its receptor. The inhibitor is used for the treatment of hypercalcemic crisis, such as that associated with a malignant tumour.
                                                                       The present invention describes compositions for the treatment of cachexia containing a substance which inhibits the binding of a parathyroid hormone related peptide (PTHTP) to its receptor, as an active component. This substance may be an antagonist to the receptor, or an antibody (preferably monoclonal) or antibody fragment, recognising PTHTP. The antibody is preferably humanised or chimeric. The present invention also describes a humanised antibody prepared by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for the treatment of cachexia arising in connection with diseases such as cancer, thereby improving the quality of life of the patient. The present sequence represents a human antibody heavy chain from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of treatment of hypercalcemic crisis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of hypercalcemic crisis with a substance inhibiting binding of parathyroid hormone related peptide to its receptor
                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                receptor - useful for, e.g. treatment of cachexia arising from cancer or other diseases
                                                                                                                                                                                                                                                                                                                      85.0%; Score 523.5; DB 20;
87.3%; Pred. No. 7.1e-41;
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                                             81; 125pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY77512 standard; Protein; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 103; Conser
                                                                                                                                                                                                                                             present invention.
                                             Page
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                                             Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77512;
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                                                                                                                                                                                                          parathormone related peptides (hPTRR). The antibodies comprise chimeric L and/or H chains, where the C region is of human and L region of mouse, origin. The present sequence represents a specifically claimed region of an antibody of the invention. Host cells, transformed with vectors containing DNA encoding antibodies of the invention, can be used to produce the antibodies. The antibodies may be used to treat hypercalcaemia, especially that due to a malignancy, e.g. cancers of pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver, breast, kidney, bladder, womb or prostate or malignant lymphoma. They may also be used for treatment of hypophosphaemia such as that due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                     New chimeric antibodies against human parathormone related peptide(s) - useful for, e.g. treatment of hypercalcaemia and other disorders caused by malignant neoplasm(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parathyroid hormone related protein; PTHrP; cachexia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibitors of binding of parathyroid hormone related peptide to its
                                                                                                                                                                                                 New antibodies have been developed which are specific for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 19; Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 523.5;
Pred. No. 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human antibody heavy chain mature protein.
                                                                                                                                                                                                                                                                                                                                                                  pathogens or to vitamin D resistance
                                                                                                                                                                 Claim 21; Page 120; 182pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW89636 standard; Protein; 118
                                            Yabuta N;
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ilarity 87.3%;
Conservative
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              (CHUS ) CHUGAI SEIYAKU KK.
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                                         Wakahara Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibitor; humanised
                                                                       WPI; 1998-230640/20
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Best Local Similarity
Matches 103; Conserv
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                                          Sato K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin; monoclonal antibody; antidiarhet; antidemetic; antidiabetic; antidiabetic; antidyretic; cancer; dehydration; excessive unination; thirst; vomiting; diarrhoea; fever; perspiration; diabetes.
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibitor of parathyroid hormone related peptide binding to its receptor can ameliorate symptoms caused by a decrease in vasopressin level due to cancer
                                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
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                                                                                                                                                                                                                                                                                                 61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGS-FAYWGQGTTVTVSS 117
                                                                                                                                                                                                      1;
                                                                         Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human antibody H chain Cregion C gamma 1 protein SEQ ID NO:56.
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                                                                         DB 21;
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                                                                      Score 523.5; D
Pred. No. 7.1e-
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB76890 standard; Protein; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000; 2000WO-JP04413.
                                                                      Query Match 85.0%;
Best Local Similarity 87.3%;
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 AA;
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Indels

Length 118;

DB 22;

Score 523.5; DB 22; Pred. No. 7.1e-41; 4; Mismatches 10;

85.0%; 87.3%;

Matches 103; Conservative

Query Match Best Local Similarity

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The present invention describes an agent (I) for the treatment and prevention of diseases other than hypercalcaemia associated with parabhyoid hormone (PTH) or parathyoid hormone related peptide (PTHP).

[I) contains as an active component a substance which promotes or inhibits the binding of ligands to PTH receptor or PTHrP receptor, or is an agonist to an agonist to these receptors. (I) have analgesic, immunosuppressive, nootropic, neuroprotective, antiinflammatory, cytostatic, antithyroid, eating-disorders and cardiovascular activities.

[I) is used for treatment and prevention of disorders associated with PTH or part.Pr., including: pain; immune suppression; disturbances of the disestive system, protein metabolism, sugar metabolism, lipid metabolism, appetite, blood chemistry, thyroid function, and electrolyte balance; central nervous system disorders such as sleep disturbance; neurological disturbances, brain function disturbance, brain circulation disturbance and autonomic nervous system disturbance, brain circulation disturbance and autonomic activities cascade including blood poisoning, dropsy, prince the present of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parathyroid hormone related peptide; analgesic; immunosuppressive; nootropic; neuroprotective; antiinflammatory; cytostatic; antithyroid; eating-disorder; cardiovascular; pain; immune suppression; appetite; digestive system; protein metabolism; sugar metabolism; lipid metabolism; blood chemistry; thyroid function; electrolyte balance; neurological; central nervous system disorder; sleep disturbance; brain function; brain circulation; autonomic nervous system; blood poisoning; dropsy; inflammation; blood disease; calcium disturbance; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation, blood disease, calcium disturbance and autoimmune disease. Treatment and prevention of disorders other than hypercalcaemia which are associated with PTH or PTHrP, especially those associated with malignant tumours, and thereby ameliorating the quality of life of these patients. AAF69141 to AAF69196 and AAB76898 to AAB76916 represent
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9
                                                                                                              61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGS-FAYWGQGTTVTVSS 117
                                                                                                                                              Human antibody H chain Cregion C gamma 1 protein SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; mouse; hypercalcaemia; parathyroid hormone; PTH; PTHrP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parathyroid hormone related peptide; gastrointestinal; cancer; central nervous system; calcium-antagonist; bone resorption inhibitor; bisphosphonate; calcitonin; calcium elimination promoter; intestinal calcium absorption inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an agent (I) for the treatment of drug-resistant hyperglycaemia. (I) contains as an active component a substance which inhibits the binding of parathyroid hormone related peptide (PPHPP) to its receptor. (I) is a calcium-antagonist. (I) can be used for treatment of drug-resistant hyperglycaemia e.g. associated with cancer. The hyperglycaemia is resistant to treatment with other drugs including bone resorption inhibitors (such as bisphosphonate or calcitonin), calcium elimination promoters and intestinal calcium absorption inhibitors. AAR69197 to AAR69252 and AAB76917 to AAB76935 represent sequences used in the exemplification of the present
                                                                                                                                                       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                       1; Gaps
                                                                                                                                                                                         1 qvqlvesgggvvqpgrs1r1scaasgftfssygmswvrqapgkglewvatissggsytyy 60
                                                                                                                                                                                                                           61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGS-FAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                             Human; mouse; drug-resistant hyperglycaemia; PTHrP; cardiovascular;
sequences used in the exemplification of the present invention.
                                                                                     DB 22; Length 118;
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                                                                                                                       Indels
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                                                                                    85.0%; Score 523.5; DB 2
87.3%; Pred. No. 7.1e-41;
ive 4; Mismatches 10
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                                                                                  Query Match 85.0
Best Local Similarity 87.3
Matches 103; Conservative
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85.0%; ilarity 87.3%; Conservative

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Length 139;
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APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: ceriani Dr., Roberto L.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129, 930B
FILING DATE: September 30, 1993
CLASSITCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: AMACEL Ph.D., VIVIAINA
REGISTRATION NUMBER: 30, 930
REFERENCE/DOCKET NUMBER: GRECC-008A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 517.5; DB 1;
Pred. No. 7.4e-46;
6; Mismatches 11;
                                                   US-08-760-8408-22
US-08-266-119-22
US-08-428-197-20
US-08-619-491-8
US-08-619-491-8
US-08-619-491-8
US-08-619-491-8
US-08-619-558-44
US-08-652-558-46
US-08-652-558-46
US-08-919-22
US-08-919-24
US-08-9197-24
US-08-428-197-24
US-08-428-197-24
US-08-428-197-24
US-08-428-197-28
US-08-428-197-28
                   US-08-437-642B-4
US-08-207-996-22
                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-08-129-930B-96
'Sequence 96, Application US/08129930B
'Patent No. 5804187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96:
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Best Local Similarity 83.3%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (510) 521-13
TELEFAX: (510) 521-3541
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 ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-129-930B-96
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 LENGTH:
TYPE:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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95.712 Million cell updates/sec
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Sequence 43,
Sequence 11,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-979-899-6
US-08-979-378A-20
PCT-US96-13152-4
US-07-934-373C-21
US-08-478-210-21
US-08-478-210-21
US-08-053-171-12
US-08-053-171-12
US-08-053-171-12
US-08-053-171-12
US-08-053-171-12
US-08-053-171-12
US-08-752-693A-4
PCT-US93-08435-13
US-08-331-398A-46
US-08-331-398A-46
US-08-313-398A-46
US-08-759-804A-46
US-08-313-398A-46
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US-08-313-398A-46
US-08-31-398A-46
US-08-31-398A-46
US-08-31-398A-46
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US-08-759-804A-46
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US-08-428-197-1
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US-08-983-607-36
US-08-665-202-30
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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RESULT 4
PCT-US96-13152-4
                                                                                                                 COUNTRY:
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                                                                                                 61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGS---FAYWGQGTTVTVSS 117
                  20 EVQMVESGGGLVQPGGSLRLSCAASGFAFSSYAMSWVRQAPGKGLEWVAEISSGGNYAYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
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Sequence 20, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE-OF INVENTION: Humanized Antibodies Reactive with
                                                                                                                                                                                                                                                                      APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
CORRESPONDENCE: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 6
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Pred. No. 1.1e-44;
6; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMFUTER: IBM PC compatible
ODFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                       US-08-974-899-6; Sequence 6, Application US/08974899; Patent No. 6037454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
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Best Local Similarity 83.8%;
Matches 98; Conservative
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CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
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Sequence 4, Application PC/TUS9613152
Sequence 4, Application PC/TUS9613152
Sequence 4, Application:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pelfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
STRIE: New York
COUNTRY: U.S.A.
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Best Local Similarity 83.8%; Pred. No. 1.9e-44;
Matches 98; Conservative 8; Mismatches 10; Indels
                                                                          ADDRESSEE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                           COMPOUTE: TITLE TOOPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                           7, VE
27-DEC-1995
27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: E95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: EPFLICATION NUMBER: EPFLICATION NUMBER: EPFLING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-00V-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
    L-Selectin
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 135 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: L-:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                       San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                          94105
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61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNY----GSFAYWGQGTTVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 502.5; DB 2;
Pred. No. 2.2e-44;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
JABER: PCT/US92/05126
15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US92/05126 FILING DATE: 15-JUN-1992
                                                                                                                                                                               P0709P2
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US-08-437-642B-21
is Sequence 21, Application US/08437642B
is Patent No. 6054297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
                                                                               FILING DATE: 14-UNW-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-1994
TELEFAX: 650/752-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
                                                                    07/715272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               81.6%;
80.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.65
Best Local Similarity 80.35
Matches 98; Conservative
                         FILING DATE: 15-JUN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear
US-07-934-373C-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 SS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCARDYDGYFDYWGQCTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 503.5; DB 5; Length 443;
Pred. No. 7.7e-44;
8; Mismatches 10; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Norman D. Hanson
RECISTRATION NUMBER: 30,946
REFERENCE/DOCKST NUMBER: BOER 1059-PCT-PEF/NDH
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-934-373C-21
Sequence 21, Application US/07934373C
Patent No. 5821373.
Patent No. 5821373.
Patent No. 5821373.
Patent No. 5821373.
APPLICANT: Paul J. Carter
APPLICANT: Peonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               PROR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILLIG DAFE: 21-Aug-1992
                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JORRESPONDE...
ADDRESSEE: General STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.7%;
83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.89
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                        FILING DATE:
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61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNY-----GSFAYWGQGTTVTV 115
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                                                                                                                                                                                                                                                        Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BR55-2 Antibody, Heavy Chain Variant
H-hu-BR55-2/1"
                                                                                                                                                    Score 502.5; DB 5; Length
Pred. No. 2.2e-44;
7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08053171
Fatent No. 5562903
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourle and Crew;
STREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Sequence of Humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                          81.6%; Scc. 80.3%; Pred. No. 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 326-240
TELEFAX: (415) 326-242
INFORMATION FOR SEQ.ID NO: 12:
                                         : 122 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                    Query Match
Best Local Similarity 80.33
Matches 98; Conservative
 INFORMATION FOR SEQ ID NO:
                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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NO
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..119
OTHER INFORMATION:
Patent No. 5562903
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
LOCATION: 1..119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
                                                         ; TYPE: amir; TOPOLOGY: PCT-US93-07832-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                       116 SS 117
                                                                                                                                                                                                                                                                                                                                                                                                                 121 SS 122
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US-08-053-171-12
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                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                             Length 122;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                             2.2e-44;
12;
                                                                                                                                                                                                                                                                                                         Ouery Match 81.6%; Score 502.5; DB 3; Best Local Similarity 80.3%; Pred. No. 2.2e-44; Matches 98; Conservative 7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application PC/TUS9307832
GENERAL INFORMATION:
    TITLE OF INFORMATION:
    TITLE OF INFORMATION: Immunoglobulin Variants
    NUMBER OF SEQUENCES: 40
    CORRESPONDENCE ADDRESS:
    ADDRESSE Genentech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IPP COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                 NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
FELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
APPLICATION NUMBER: 07/934373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
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                                                                                                                                                              TYPE: Amino Acid
TOPOLOGY: 1:12
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
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910/371-7168
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                                                                                                                                                                                                                                                    US-08-437-642B-21
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TELEX: 9
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61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHN---YGSFAY-----WGQGTT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Newman, Roland A.
APPLICANT: Newman, Nabil
APPLICANT: Ranab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BORNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STRATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            Score 502; DB 1; Length 125;
Pred. No. 2.5e-44;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCETAMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A FILING DATE: US/08/101995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING APPLICATION DATA:
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATFORNEY/AGENT INFORMATION:
NAME: Teskin ESQ., Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US 07/856,281
23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 99, Application US/08476349A Patent No. 5750105 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                      | LENGTH: 125 amino acids | TYPE: amino acids | TYPE: amino acid | STRANDEDNESS: not relevant | TOPOLOGY: not relevant | MOLECULE TYPE: peptide | POSITION IN GENOME: | CHROMOSOME/SEGMENT: 18/2 | US-08-478-039-99
                                                                                  SS: not relevant not relevant
                                                                                                                                                                                                                                                               81.5%;
79.2%;
    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               Query Match 81.5
Best Local Similarity 79.2
Matches 99; Conservative
                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 VTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-HNYGS-FAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 99, Application US/08478039
Fatent No. 5681722
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Naman, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                         81.5%; Score 502; DB 1; Length 119;
81.5%; Pred. No. 2.4e-44;
iive 13; Mismatches 7; Indels
  /note= "Complementarity-determining
                                                                                                                                                                                                  /note= "Complementarity-determining region"
                                                                                                      /note= "Complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 23-AMR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN ESQ., ROBIN L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                    region"
                                                                                                                               region"
                                                                                                                                                                                                                                                                                                                                                                      97; Conservative
                                                            NAME/KEY: Region
LOCATION: 50..66
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                         LOCATION: 99.108
COTHER INFORMATION:
COTHER INFORMATION:
US-08-053-171-12
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                       NAME/KEY: Region
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Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                 FEATURE:
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Query Match
Best Local Similarity 82.1:
Matches 96; Conservative
                                                                                                                                                                                                                                           NAME/KEY: heavy chain US-08-983-607-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                           DESCRIPTION:
ORIGINAL SOURCE:
                                                                                                                                                                                                      CLONE: V13
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                                                                                                                                                                                                                                                                                                                                                                  81.5%; Score 502; DB 1; Length 125; 79.2%; Pred. No. 2.5e-44;
Live 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: APTIL 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARY M. Krinsky
REGISTRATION NUMBER: 32423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 06520-8114
                                                        LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 266 Whitney Avenue CITY: New Haven STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: OC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                 Best Local Similarity 79.29
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 203-773-954
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: $EQUENCE CHARACTERISTICS:
LENGTH: 131 residues
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 131 residues
amino acid
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1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 131;
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MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1.5 inch 1.44 Mb storage diskette
COMPUTER: 1.6 inch 1.44 Mb storage dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA USING HUMANIZED ANTIBODIES WHICH BIND TO ANTIGEN A33
                                                                                                ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 500.5; DB 4;
Pred. No. 3.7e-44;
                                                                                                                                                                                                                                                                                                                      LIBRARY: DM414 scFv antibodies obtained from LIBRARY: fUSE5 fusion phage construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US96/07321
FILING DATE: May 21, 1996
APPLICATION NUMBER: 08/02,23
FILING DATE: FEDENARY 16, 1993
APPLICATION NUMBER: 07/673,153
FILING DATE: MARCH 18, 1991
APPLICATION NUMBER: 07/327,765
FILING DATE: MARCH 23, 1989
APPLICATION NUMBER: 07/118,411
FILING DATE: No. 6190640ember 6, 1987
FILING DATE: APPLICATION NUMBER: 06/724,991
FILING DATE: APPLI 19, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.2%; Scor.
82.1%; Pred. No. 3...
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clarence William Jr.
Elizabeth Carswell Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08752693A
Patent No. 6190640
GENERAL INFORMATION:
APPLICANT: Sydney Welt
Gerd Ritter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leonard Cohen
polypeptide
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5,

Gaps

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61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---HNYGSFA--YWGQGTTVTV 115
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smithfile Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
ITILE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
                                                                                                                                                                                                                                                         1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                      Length 122;
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                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              11;
                                                                                                                                                                      DB 5;
                                                                                                                                                                    Query Match 80.8%; Score 497.5; DB Best Local Similarity 79.5%; Pred. No. 7e-44; Matches 97; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.8%; Score 497.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application PC/TUS9308435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 540-2200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                    LENGTH: 122 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 amino acids
                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-08435-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: U. S. Government, Secretary of
APPLICANT: The Navy
APPLICANT: The Navy
APPLICANT: The Navy
APPLICANT: The Secretary of
APPLICANT: The Secretary of
APPLICANT: The ARMY
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             81.2%; Score 500; DB 4; Length 117;
80.3%; Pred. No. 3.7e-44;
Live 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolease #1.0, Version #1.25
APPLICATION NAMBER: PCT/US93/08435
               NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human A33
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SBC P50107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: <URKNOWN>
DESCRIPTION: SEQ ID NO:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
ATTORNEY/AGENT INFORMATION
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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Matches 94; Conservative
                                                                                                                                                                                             LENGTH: 117
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    80.3%; Pred. No. 7e-44;
Live 7; Mismatches 12; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,925
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APPLICANT: Bolt, Sarah L
APPLICANT: Clark, Michael R
APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: antibody preparation
WHMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye pc
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 7038164000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
Best Local Similarity 80.3
Matches 98; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
US-07-988-925-11
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MEDIUM TYPE: Floppy
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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gb_pl2:*
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AX060782 Sequence AX060810 Sequence AX060786 Sequence M95943 Mouse mRNA M35667 Mouse 1ysoz M3959 Mouse Ig ac AR163757 Mus muscu M95945 Mouse muscu

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Description

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1 (bases 1 to 321)
Huse, W.D. and Wu, H.
Anti-g(a) v?_g(b) 37 recombinant human antibodies, nucleic acids
enceding same and methods of use
Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
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    /organism="synthetic construct"
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| AF139844
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AX060782.1 GI:12406162
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1 (bases 1 to 321)
Huse, W.D. and Wu.H.
Anti-g(a) v?-g(b)37 recombinant human antibodies, nucleic acids encoding same and methods of use Patent: WO 0078815-A 31 28-DEC-2000;
Applied Molecular Evolution (US)
                                                                                                                                                                                                         61 CTTCCTGCCAGGCCAGCCAAAGTATAGCAACCACCTACACTGGTATCAACAAAAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                  240
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                                             Gaps
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Pred. No. 4.8e-89;
0; Mismatches 3; Indels
                                             Indels
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/note="grafted antibody variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
Ouery Match 100.0%; Score 321; DB 9; Best Local Similarity 100.0%; Pred. No. 5.4e-90; Matches 321; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
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Sequence 31 from Patent WO0078815.
AX060810
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Best Local Similarity
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DEFINITION ACCESSION VERSION

RESULT AX060786 LOCUS

ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE

JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 321) Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S., Co,M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L.
                                                                                                                                                                           Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSIGRACY 321 bp mRNA ROD 27-APR-1993 Mouse lysozyme-binding Ig kappa chain (HYHEL-10) V23-J2 region mRNA, partial cds.
M3567 I GI:196584 immunoglobulin-kappa; processed gene; variable region VK23.
MOUSE Hybridoma, CDNA to mRNA, clone 10K-106.
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                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="MAb 33"
/cell_type="hybridoma"
1. .321
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                    1. .321
/organism="Mus musculus"
/strain="BALB/c"
                                                                                 Mouse mRNA sequence, partial cds. M95943
                                                                                                                                                                                                                                                                                                                   Unpublished (1992)
Location/Qualifiers
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301 GGGACCAAGCTGGAAATTAAG 321
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86.2%;
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Best Local Similarity 86.2
Matches 276; Conservative
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| Mo_xref="G1:1240617"
| /translation="DIVIDOSPALSYPEDSVSLSCQASOSISNHLHWYQQKSHESP
| /translation="DIVIDOSPALSYPEDSVSLSCQASOSISNHLHWYQQKSHESP
RLIKYRSQSISGIPSRFSGSGSGTDFALSINSVETEDFGWYFCQQSGSWPHTFGGGT
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmanla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muse, W.D. 1 (bases 1 to 321)

Huse, W.D. and Wu, H.

Anti-_g(a) V2_g(b) 37 recombinant human antibodies, nucleic acids encoding same and methods of use

Patent: WO 0078815-A 7 28-DEC-2000;

Applied Molecular Evolution (US)
                                                                                 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACAGGTATCAACAAAAGGCCT 120
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                AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
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Pred. No. 2.1e-73;
0; Mismatches 33; Indels 0
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                                                                                                                                                                                                                                                                    AAVU6U786 321 bp DNA
Sequence 7 from Patent WO0078815.
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/db_xref="taxon:10090"
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Best Local Similarity 89.7
Matches 288; Conservative
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/protein_id="aAA38741.1"
/prote
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Nucleotide sequences of immunoglobulin heavy and light chain
V-regions from a monoclonal autoantibody specific for a unique set
of small nuclear ribonucleoprotein complexes

Nucleic Acids Res. 20, 4099-4099 (1992)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla; Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus.
I (bases, 1 to 321)
Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and
Brooks, W.B.R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 370)
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                                                                                                                                                                                                                                                                                                                        <1._.>321
/note="lysozyme binding Ig kappa chain V23-J2 region"
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Pred. No. 1.4e-67;
0; Mismatches 44; Indels 0;
                                                                                                                            A three-dimensional model of an anti-lysozyme antibody J. Mol. Biol. 194, 713-724 (1987)
88011212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ייטיבעאאט 370 bp mRNA ROD
Mouse Ig active kappa-chain V-region, partial cds.
M93959

    .321
    /organism="Mus musculus"

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                                                                                                                                                                                                                    Location/Qualifiers
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Mus musculus cDNA to mRNA.
Mus musculus
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86.2%;
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MEDLINE
FEATURES
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/INDICLION valiance restant
/product="inmunoglobblin kappa-chain"
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LHWYQOKSHESPRLIKYVSQSISGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQ
SNSWPHTFGSGTKLEIKRADA"

9 0 c 86 g 98 t
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Mus musculus mAb 101.4.1 immunoglobulin light chain variable region
MRNA, partial cds.
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Metrens, M. M., Gallvin, J.E., Adderson, E.E. and Cunningham, M. W.
Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
Mouse Monoclonal Antibodies
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mertens,N.M. and Cunningham,M.W.
Direct Submission
Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 CATGAGTCTCCAAGGCTTCTCATCAAGTATGTTTCCCAGTCCATCTCTGGGATCCCTCC 216
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Pred. No. 1.4e-67;
0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                               /codon_start=1
/function="variable region"
/organism="Mus musculus"
                  /db_xref="taxon:10090"
/map="6"
                                                                                                                                                                                                       /note="putative"
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                                                                                            /gene="IgK"
1.370
/partial
/gene="IgK"
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86.2%;
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E07933 381 bp RNA PAT 29-SEP-1997
CDNA encoding variable region of mouse anti-FHV-1 antibody L chain.
E07933
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1. 381
/product='variable region of mouse anti-FHV-1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y. .
ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT
ENCODING THE SAME ANTIBODY
PATENT: JP 1994217786-A 2 09-AUG-1994;
CHEMO SERO THERAPEUT RES INST
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KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAWA KIYOTO, PI
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                                                                                Score 248; DB 94; Length 321;
Pred. No. 4.6e-67;
0; Mismatches 45; Indels (
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1. .381
/organism="Mus sp."
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/note="putative"
79 c 77
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JP 1994217786-A/2
09-AUG-1994
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hypothetical: No;
                                                                                    77.3%;
85.9%;
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JP 1994217786-A/2.
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                                                                                                      Best Local Similarity 85.9
Matches 275; Conservative
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CO (12P21/08, AP
CC strandedness
CC topology: L.
CC hypothetical
CC anti-sense:
FH Key
FH Source
FT source
FT mat_peptide
FT
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Mus sp.
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KEYWORDS
SOURCE
ORGANISM
                BASE COUNT
ORIGIN
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TITLE
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                                                                                                                                   /codon_start=1
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RLLIXYASQSISGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQSNSWPLTFGAGT
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Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S., Co, M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L. Untitled Unpublished (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA. Mus musculus
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Pred. No. 4.6e-67;
0; Mismatches 45; Indels (
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/db_xref="taxon:10090"
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    321
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    .321
    /organism="Mus musculus"

                                                            /strain="BALB/c"
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/note="mab 101.4.1"
<1. .>321
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                Location/Qualifiers
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1 (bases 1 to 381)
Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelingh,K.L.
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                              GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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1 (bases 1 to 381)
Queen.C.L., Schneider,W.P. and Selick,H.E.
Polynucleotides encoding improved humanized
Patent: US 5693761-A 82 02-DEC-1997;
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85.9%; Pred. No. 4.6e-67;
ive 0; Mismatches 45;
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178626.1 GI:3014780
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Matches 275; Conservative
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                                                                     Score 248; DB 10;
Pred. No. 4.6e-67;
0; Mismatches 45;
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Queen, C.L. and Selick, H.E.
Humanized immunoglobulins
Patent: US 5585089-A 82 17-DEC-1996,
Location/Qualifiers
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/db_xref="taxon:10095"
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131959.1 GI:1822750
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/cell_type="B cell hybridoma (spontaneous fusion with
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M19913 J03832
M19913.1 G1:197033
C-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 56)
Rule G.S.
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Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
bodies for NMR studies
Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
B834486
Draft entry and computer-readable sequence [2] kindly submitted by
G.Rule, 20-JUL-1988.
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Pred. No. 4.6e-67;
0; Mismatches 45
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/cell_type="mature B cell"
            Humanized immunoglobulins
Patent: US 5693762-A 82 02-DEC-1997;
Location/Qualifiers
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                 Query Match 77.3%;
Best Local Similarity 85.9%;
Matches 275; Conservative
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and Selick, H.E.
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93. .>431. .>431. ...
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Brard, F., Shannon, M., Prak, E.L., Litwin, S. and Weigert, M. Somatic mutation and light chain rearrangement generate autoimmunity in anti-single-stranded DNA transgenic MEL/lpr mice 94406777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-APR-1999) Molecular Biology, Princeton University, Washington Road, Room 401, Princeton, NJ 08544, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF139844 324 bp mRNA ROD 04-NOV-1999
Mus musculus clone 50 immunoglobulin kappa light chain variable
region Vk23 (IGG) mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 324)
Brard, F. and Weigert, M.
Direct Submission
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Vk23"
Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M. Somatic mutation and light chain rearrangement generate autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice 99406777
                                                                                            2 (bases 1 to 324)
Brand,F. and Weigert,M.
Direct Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                               /cell_type="B cell hybridoma (spontaneous fusion with SP2/0]"
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/gene="195"
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148. 168
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/note="CDR2; complementarity determining region
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/organism="Mus musculus"
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Pred. No. 1.5e-66;
0; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                       /note="variable region (VJ)"
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                                                                                                                                                                                                                                                                                                                                    /tissue_type="spleen"
<1. .>324
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85.6%;
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                                                                                                                   /product-"immunoglobulin kappa light chain variable region
Vk23"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
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Pred. No. 1.5e-66;
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Best Local Similarity 85.6%;
Matches 274; Conservative
                                                                                                 /gene="IgG"
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                                                                                                        October 11, 2001, 14:33:59; Search time 2341.88 Seconds (without alignments) 1295.697 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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117; gb_est48;*
118; gb_est48;*
119; gb_est50;*
120; gb_est51;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.	Cidne distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.lln.gov Plate: LiAM9GOI row: f column: 11 High quality sequence stop: 714. High quality sequence stop: 714. FEATURES 1. 738 Location/Qualifiers 1. 738 Ab.xref="taxon:10090" / Strain="rybk" / Ab.xref="taxon:10090" / Clone="Inba" NCI_CGAP_CO24" / Ab.host="DH10B (T1 phage-resistant)"	Query Match 68.4%; Score 219.6; DB 150; Length 738; Best Local Similarity 84.9%; Pred. No. 1.4e-57; Agps 270; Conservative 0; Mismatches 44; Indels 4; Caps 27; Qy 6 TGTGCTAACTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACTCTTTC 65 111111111111111111111111111111111111	126 AGCCCAAGGCTTCTCATCAACTATCCTTCCAACTCTGGGATCCCGCCAGGTT	BF579007 945 MRNA Sequence. BF579007 BF579007 BF579007 BF579007 BF579007 BF579007 BF779007 B
Result Query No. Score Match Length DB ID Description	1 219.6 68.4 738 150 BF592153 602099743 2 214 66.7 949 150 BF579007 602096124 3 206.4 64.3 946 155 B659760 AM406486 AM406486 UI-F-BLO 4 206 64.2 434 115 AM4065486 AM406486 UI-F-BLO 5 203.2 63.3 398 115 AM405309 UI-F-BLO 6 201.6 62.8 519 115 AM405183 AM4051309 UI-F-BLO 8 201.6 62.8 519 115 AM405183 AM4051309 UI-F-BLO 9 201.2 62.7 385 115 AM405691 AM405610 UI-F-BLO 10 200 62.3 468 115 AM405643 AM405605 UI-HF-BLO 11 198.4 61.8 1015 155 BG536848 BG536848 BG536848 BG536848 BG536848 BG536848 </td <td>191.8 59.8 461 115 MW406219 191.8 59.8 1061 115 BF5633521 190.8 59.4 330 115 AW406212 180.8 59.1 413 115 AW406440 189.6 59.1 413 115 AW406057 188 58.8 409 115 AW406057 188 58.6 639 32 AV734416 188 58.6 639 32 AV734416 187.2 58.3 448 115 AW405460 186.2 58.9 468 115 AW405460 186.2 58.9 468 115 AW405460</td> <td>185.8 57.9 317 115 AW404261 AW404261 185.6 57.8 748 154 BG529887 BG52987 BG52943 BG52943 BG52943 BG52943 BG52943 BG52943 BG52943 BG52943 BG53947 BG545397 BG545546 BG</td> <td>RESULT 1 BF582153 738 bp mRNA EST 12-DEC-2000 DEFINITION 602099743F1 NCI_CGAP_CO24 Mus musculus CDNA clone IMAGE:4219402 5', ACCESSION BF582153 GI:11655865 EST 12-DEC-2000 NERWONDS ST 101:11655865 EST 12-DEC-2000 NERWONDS ST 101:11655865 EST 12-DEC-2000 NERWONDS ST 101:11655865 EST 12-DEC-2000 LEAST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-</td>	191.8 59.8 461 115 MW406219 191.8 59.8 1061 115 BF5633521 190.8 59.4 330 115 AW406212 180.8 59.1 413 115 AW406440 189.6 59.1 413 115 AW406057 188 58.8 409 115 AW406057 188 58.6 639 32 AV734416 188 58.6 639 32 AV734416 187.2 58.3 448 115 AW405460 186.2 58.9 468 115 AW405460 186.2 58.9 468 115 AW405460	185.8 57.9 317 115 AW404261 AW404261 185.6 57.8 748 154 BG529887 BG52987 BG52943 BG52943 BG52943 BG52943 BG52943 BG52943 BG52943 BG52943 BG53947 BG545397 BG545546 BG	RESULT 1 BF582153 738 bp mRNA EST 12-DEC-2000 DEFINITION 602099743F1 NCI_CGAP_CO24 Mus musculus CDNA clone IMAGE:4219402 5', ACCESSION BF582153 GI:11655865 EST 12-DEC-2000 NERWONDS ST 101:11655865 EST 12-DEC-2000 NERWONDS ST 101:11655865 EST 12-DEC-2000 NERWONDS ST 101:11655865 EST 12-DEC-2000 LEAST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-2000 EST 12-DEC-2000 LEAST 12-DEC-2000 EST 12-DEC-

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/Organism="Name sapiess"
//Ob_xref="taxon:9606"
/clone="IMAGE:4717049"
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Sfil (ggcgcctctggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCCGACGCGCGCGACATG (T30)BN-3' (where B = A,
C, or G and M = A, C, G, or T) Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MC Library."
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1566 row: e column: 18

High quality sequence stop: 738.
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="InAGE:4216180"
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Site_2: S3I; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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1 (bases 1 to 946)

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
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                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.p column: 05
Plate: LLAM9792 row: p column: 05
High quality sequence start: 9
High quality sequence stop: 730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCTGGTGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 AGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCCAGGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 TTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGGGGGAC 305
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    Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 434)
NIH-MGC http://mgc.ncl.nih.gov/.
                                                                                                                         96 GAAATICGTGTTGACACAGTCTCCAGCCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACC 155
                                                                                                                                                                                             61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                             121 GGTCAAGCCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                             1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCCAGGAGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UI-HF-BL0-acr-f-12-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060238 5', mRNA sequence.
                                                                                                                                                                                                                         181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 946;
                                               ö
Score 206.4; DB 155; Lengt
Pred. No. 2e-53;
0; Mismatches 71; Indels
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can be

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Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
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AV733856 cdA Homo sapiens cDNA clone cdABAH01 5', mRNA sequence.
AV733856
      1 (bases 1 to 398)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                          Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Email: cgapbs-remail.nih.gov.
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 115; Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_wref="taxon:96f06"
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/cell_type="typmph"
/cell_line="MGC95"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 203.2; DB Pred. No. 1.5e-52.0; Mismatches 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Best Local Similarity 77.2%;
Matches 247; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:3060238"
/clone="INAGE:3060238"
/clone="type="1ymph"
/cell_type="germinal center B cells"
/cell_line="MGG86"
/lab_host="DH108 [LTI]"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1: NotI; Site_1
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CLONG distribution: M.G. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M.B. Roward
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.1e-53;
0; Mismatches 70;
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AW405309.1 GI:6924366
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Best Local Similarity 78.0%;
Matches 248; Conservative
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Gaps

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/note="Vector: prir3-Pac; Site_1: Not1; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaido, Ph.D. and M. Bento Soares, Ph.D."
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BE306691.1 GI:9160297
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Enail: cgapbs-rémail.nih.gov
Enc Ni site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.8%; Score 201.6; DB 115; Length 519; 76.9%; Pred. No. 5.2e-52; O: Mismatches 74; Indels O;
                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="lymph"
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                                                                                                                                                                                                                                                                                                  / S19
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                        Unpublished (1999)
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Matches 246; Conservative
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                                      Yang,Y., Song,H., Peng,Y., Gu,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,Y., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 519)
                                                                                                                                                                     Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB" 152 c 122 g 111 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CTTTCCTGCCAGGCCAGGCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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AW405183 GI:6924240
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 201.6; DB 32; Length 482;
Pred. No. 5.1e-52;
0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                  Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="cdABAH01"
/clone_lib="cdA"
/clone_type="phecohromocytoma"
/dev_stage="Adult"
/lab_nost="BM25.8"
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ilarity 76.9%;
Conservative 0
                      (bases 1 to 482)
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/note="Vector: pryr3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (L15-2:Skb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Exe II site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward
                        1 (bases 1 to 385)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TTCCTGCCAGGCCAGCCAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCTGG 122
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1 (bases 1 to 385)
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/cell_line="MGC85"
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1. .385
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            NIH MGC http://mgc.nci.nih.gov/.

NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM8561 row: g column: 20

High quality sequence stop: 598.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary./tissue_cil origin."
/lab_host-"DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 166; Length 624;
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Pred. No. 5.5e-52;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                  1. .624
/organism="Mus musculus"
/strain="CzECH II (feral)"
/db_rref="trach:10090"
/clone="IMAGE:3501355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.8%;
Best Local Similarity 76.9%;
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
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Best Local (
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BASE COUNT ORIGIN

61

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RESULT AW405025

ACCESSION

VERSION KEYWORDS SOURCE

301

359

ORGANISM

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Gaps

126 182 186 242

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: prectionally conned." Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
a 137 c 114 g 111 t
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                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 468) NIH WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                               information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 198.4; DB 115; Length 468;
Pred. No. 5e-51;
0; Mismatches 76; Indels 0;
                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco Ri site shown at the beginning of the sequence.
Fissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution informa
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.11n1.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_37"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 GGGACCAAGCTGGAGATCAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244; Conservative
                                                                                                                                                                                      Unpublished (1999
                                   Homo sapiens
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                                ORGANISM
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ORIGIN
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COMMENT
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                                                                                                                                  AUTHORS
TITLE
                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="bH108 [LTI]"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(l.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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0
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 468)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                        Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llni.gov/bbrp/image.html

Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
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AW404506 II.6923563
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Pred. No. 1.6e-51;
0; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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illarity 76.6%;
Conservative
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TITLE
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                                                                                                         ACCESSION
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                                                                                                                                     VERSION
KEYWORDS
SOURCE
AW4 04 697
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IthAGE:4691085"
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                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM1509 row: k column: 22
High quality sequence stop: 624.
                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1015)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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Pred. No. 6.4e-51;
0; Mismatches 76; Indels 0;
                      BG536848.1 GI:13528394
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76.2%;
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Matches 244; Conservative
                                                                                                         Homo sapiens
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RESULT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 11 (bases 1 to 465)
11H-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                Contact: Robert Strausberg, ph.D.

Contact: Robert Strausberg, ph.D.

Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-blo.llnl.gov/bbry/image.html

Seq primer: MI3 Forward.
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AW404697 465 bp mRNA EST 16-FEB-2000 UI-HF-BL0-acd-b-04-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058518 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens'/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                        AW404697.1 GI:6923754
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75.9%;
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Best Local Similarity
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                                                                RESULT 15
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 548)

S NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCML564 row: m column: 13

High quality sequence stop: 548.
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                                   BG568486 548 bp mRNA EST 10-APR-2001 602587455F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716468 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCCAGCTGGCCTCACACGTTCGGAGGG 300
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                                                                                          BG568486.1 GI:13576139
                                                                mRNA sequence.
BG568486
                                                                                                                                     Homo sapiens
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Matches 242; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                        human.
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Tangeries, Cardining, House, House, House, House, House, House, House, Liu, F., Qui, J., Gao, G., Xiao, H., Xu, X., Li, N., Qiao, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qui, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, Y., Ju, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Homo sapiens cDNA cdA clones
Unpublished (2000)
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
Gontact: Zequang Han
Chinese National Human Genome Center at Shanghai
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pheochromocytoma"
/dev.stage="Adult"
/lab_host="BM25.ste"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
1 148 c 118 g 120 t
                                                                                                                                                            AV734882 CdA Homo sapiens cDNA clone cdABFC04 5', mRNA sequence.
AV734882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 GAAATTGTGTTGACACAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGACCCACC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTTTCCTGCCAGCCAGCCAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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Pred. No. 1.6e-49;
0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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301 GGGACCAAGGTGGAAATTA 319
                           406 GGGACCAAGGTGGAAATCA 424
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Humanised antibody Humanised antibody

Expression vector

Murine vitronectin Plasmid pBT111 enc Mouse anti-verotox Human secreted exp cDNA encoding kapp EGF receptor chime

Perfect score:

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Scoring table:

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Database

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Light chain variab
DNA encoding the v
Anti-ILZR-beta ant
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B-BIO MAb L chain
Anti-gp54 MAb 48-1
Human Fab clone LD
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hIL2R Ab L chain V
Mouse monoclonal a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "vitaxin antibody light chain variable region" /note= "partial sequence, no start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vitaxin antibody light chain variable region DNA.
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                                          AAZ35242
AAA44346
AAT49345
AAT33446
AAD00904
AAD00906
AAZ10202
AAT38510
AAQ43245
AAD01262
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AAV71805
AAV71805
AAZ1805
AAZ10203
AAN936615
AAN930300
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AAX77408
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AAT42033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV49821 standard; DNA; 321
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Search time 177.65 Seconds (without alignments) 1134.570 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding light
LM609 antibody lig
Antibody LM609 lig
Humanised anti-ver
Humanised anti-alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitronectin alpha-
Sequence of mouse
Murine CMV5 antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vitaxin light chai
LM609 antibody lig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitaxin antibody l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **Carbassag_0001:**

**Carbass
                                                                                                                                                                                                                                                                                          1 GAGATTGTGCTAACTCAGTC......GGACCAAGGTGGAAATTAAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                          730101 seqs, 313950809 residues
                                                                                                                                                          ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                     October 11, 2001, 15:12:35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV49843
AAF28199
AAV49823
AAF28178
AAZ35244
AAV71800
AAV71802
AAQ64167
AAF58747
                                                                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV49821
AAF28176
                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_0601:*
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Match 1
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Score

Result Š. 321 321 318.6 318.6 318.2 268.2 268.2 260.8 252.8 252.8 252.8

Anti-gp54 MAb 48-î Plasmid pWW152-225 Plasmid pSW202-225

Anti-human

us-08-791-391a-3.rng

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28-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                        This sequence encodes the vitaxin antibody variable light chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 bid can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin—mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ggtcaagccccaaggcttctcatcaagtatcgttcccagtccatctctgggatccccgcc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITTCCTGCCAGGCCAAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                   sed antibody, Vitaxin, that binds selectively to alphaVbeta3
in - and related grafted antibodies based on murine monoclonal
also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 aggitcagiggcagiggatcagggacagatitcacccicaciateiccagictggagect
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                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                         Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                grafted antibody; alphaVbeta_3 integrin; angiogenesis; natory; cancer; retina; restenosis; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 321; DB 19; 100.0%; Pred. No. 1.2e-91;
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                  Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vitaxin light chain variable region DNA.
                                                                   Humanised antibody, Vitaxin, that
                                                                                                                                   Claim 6; Fig 1b; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF28176 standard; DNA; 321 BP.
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                                                                                                            angiogenesis or restenosis
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                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 321; Conservative
      Huse WD;
                               WPI; 1998-437472/37.
P-PSDB; AAW76002.
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inflammatory;
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      Glaser SM,
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                                                                                                                                                                                                                                                                                                                                                         Query Match
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of anglogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaNpeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of antibodies. The antibodies or their functional alphaNpeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psorlasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTGGGGATCCCCGCC
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                                                                                                                                       (MOLE-) APPLIED MOLECULAR EVOLUTION.
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23-JUN-2000; 2000WO-US17454
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                                                                                                                                                                                                        Wu H;
                                                                   24-JUN-1999;
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This sequence encodes a LM609 grafted antibody variable light chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, mediated degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more
Vitaxin; antibody; variable region; heavy chain; light chain; integrin, LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.
                                                                                                                                                                                                                                       /note= "partial sequence, no start or stop codon given"
                                                                                                                                                                                                   /product= "IM609 grafted antibody light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
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                                                                                                1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAGGGCGACT 60
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                                          DB 19; Length 321;
                                                                      Indels
Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
                                     Score 318.6; DB 1
Pred. No. 6.5e-91;
                                                                   2; Mismatches
                                       99.3%;
99.1%;
                                                                   Matches 318; Conservative
                                                       Similarity
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
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Pred. No. 1e-90;
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99.18;
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                                                       Matches 288; Conservative
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83
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                                            Similarity
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Sequence 321 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the LM609 antibody variable light chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically anglogenesis and restenosis (but also e.g. (non )immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                        "LM609 antibody light chain variable region" artial sequence, no start or stop codon given"
                                                                 Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
121 ggtcaagccccaaggcttctcatcnnntatcgttcccagtccatctctgggatcccgcc
                                 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                           LM609 antibody light chain variable region DNA fragment.
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                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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P-PSDB; AAW75004.
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(Y)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -
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                                                                                                                                                                                                                                                     61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                  antibodies
                                                                                                                                                                 1 gatattgtgctaactcagtctccagccaccctgtctgtgacaccaggagatagcgtcagt
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                                                                                                             1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                      121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGITCAGTGGCAGTGGATCAGGGACAGAITTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
  Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ds.
                                                         Indels
  19;
                                                         33;
Score 268.2; DB 1
Pred. No. 4.8e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody LM609 light chain variable region DNA.
                                                      0; Mismatches
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181
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                                                                                                                                                                                     ctttcctgccaggccagccaaagtattagcaaccacctacactggtatcaacaaaatca 120
                                                                                                                                                                                                       GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                         catgagtetecaaggetteteateaagtategtteecagteeatetetgggateecetee 180
                                                                                                                                                                                                                                                                               GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                         1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; light chain; mouse; human; humanised antibody;
Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
           of
                                                                                                                                                                                                                                                     AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                             .;
0
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised anti-verotoxin II antibody VTm1-1 VL cDNA.
                                                                                           DB 22;
                                                                                    Score 268.2; DB 22;
Pred. No. 4.8e-75;
                                                                Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                   301 gggaccaagctggaaattaag 321
                                                                                                                                                                                                                                                                                                                   GGGACCAAGGTGGAAATTAAG 321
                                                                                          83.6%;
89.7%;
                                                                                                                                                                                                                                                                                                                                                                                AAZ35244 standard; cDNA; 381
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                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                              Conservative
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61..381
/*tag=
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUS; therapy; ss.
                                                osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0-MAY-1998;
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                                                                                                            Matches 288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                            Query Match
                                                                                                    Local
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This DNA sequence codes for a humanised light chain variable region (see AAY33407) of murine monoclonal antibody VTm1-1 (MuVTm1-1), an antibody that specifically binds to the B subunit of verotoxin II (C VT2). The invention relates to humanised antibodies against VT2 that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVTm1-1 comprising the cc complementarity determining regions of MuVTm1-1 (see AAY32404-05) and theavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain frameworks, provided that at least 1 copsition selected from L49, H29, H30, H49 and H98 is occupied by the minor acid at the equivalent position of the MuVTm1-1 antibody heavy or light chain variable region framework. Such humanized antibodies have an affinity for VT2 that is 3-, 5 or 10-times that of MuVTm1-1. They are used for treating a patient suffering from, or at risk of, the toxic effects from VT2 (claimed), especially for treating coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).
                                                                                                                                                              used for treating Verotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 gaaattgtgctaactcagtctccagccacctgtctgtgtctccaggagaaagagccact 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
   Vasques M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTGGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 381;
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   MS,
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   Takedo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 260.8; DB 2
88.4%; Pred. No. 1.1e-72;
                                                                                                                                                           binding to verotoxin II
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   Kimura T,
                                                                                                                                                                                                                                                       Disclosure; Fig 2b; 59pp; English.
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   Imaizumi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.4*
Matches 283; Conservative
                                                           2000-086580/07
                                                                                                                                                        Humanized antibody
producing E. coli -
                                                                                            P-PSDB; AAX32407
Matsumoto Y,
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181 aggttcagtggcagtggatcagggacagatttcactctcaccatcagccgtctagagcct 240

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This DNA sequence codes for the light chain variable region (VL, see AAW84098) of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody D12HZHC 1-0. It is based on the VL sequence (see AAW84096) of human Kabat subgroup III kappa chain, with complementarity determining regions from the murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84094).

The synthetic VL humanised vit DNA sequence is also provided in the synthetic VL humanised will DNA sequence is also provided for passive immunotherapy of a disorder mediated by the alpha-v beta-3 receptor, e.g. cardiovascular disorders or angiogenic related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and restenoiss, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis, hyperparathyroidism, paget's disease, hypercalcemia of malignancy, osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex homene deficiency. They can also be used for targeted drug

    used for

                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New anti alpha_v beta_3 vitronectin receptor antibodies - used immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
                    angiogenesis; diabetic retinopathy; inflammation;
macular degeneration; osteoporosis; Paget's disease;
hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
cancer; metastasis; rheumatoid arthritis; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy, and for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                               Taylor AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 61-62; 97pp; English.
                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                         98WO-US04987.
                                                                                                                                                                                                                                                                                              97us-0039609.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW84098
                                                                              D12HZHC-10; ds
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                                                                                                                                                                         WO9840488-A1
                                                                                                                   saptens
                                                                                                                                                                                                                                                       12-MAR-1998;
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                                                                                                                                      Synthetic.
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Gaps

Score 252.8; DB 20; Length 338; Pred. No. 3.4e-70; 0; Mismatches 42; Indels 0;

Sequence 338 BP; 82 A; 99 C; 79 G; 78 T; 0 other;

diseases.

1 GAGATTGTGCTAACTCCAGTCTCCAGCCACCCTGTCTCTCAGCCCCAGGAGAAGGGCCGACT 60

δ

; 0

Query Match 78.8%; Best Local Similarity 86.9%; Matches 278; Conservative

expression

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241 GAAGATTTTGCAGTCTATTÁCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody (MAD) D12 light chain variable region (VL, see AAW85000) that is altered in humanised D12 VL (see also AAW84098), including the first 5 amino acids of the human kappa constant region. It was prepared from 4 overlapping synthetic oligonuclectides (see AAV71816-19). The synthetic gene was used to construct an expressio vector for humanised D12 VL, D12 is an anti-alpha-v beta-3 vitronectin receptor MAD. Humanised D12 MADs can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated
                                                                                                                                                                                                                                                                                                           Humanised antibody; monoclonal antibody; MAb; antibody engineering;
                  mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti alpha_v beta_3 vitronectin receptor antibodies - used immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This DNA sequence codes for the region of the murine monoclonal
                                                                                                                                                                                                                                                                           Vitronectin alpha-v beta-3 MAb VL cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 64; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                          AAV71802 standard; cDNA; 338 BP
                                                                301 GGGACCAAGGTGGAAATTAA 320
                                                                                              301 ggtaccaaggtggaaataaa 320
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                                                                                Jonak ZL,
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P-PSDB; AAW84100.
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Mus sp.
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                                                             240
                                                                                                                  300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The inventors claim a monoclonal antibody against feline herpes virus (FHV-1). They also claim a recombinant antibody against FHV-1
       1 gacatagtactgactcagtctccaggcaccctgtctttgtctccaggagaaagagccacc
                                                                                  AGGTTCAGTGGCAGTGGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                           GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                         41 gaagattttgcggtttattactgtcaacagagtaacagctggcctttcacgttcggccag
                      CTTTCCTGCCAGGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT
                                                     GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline monoclonal antibody and recombinant antibodies specific for FHV-1 - for detection, treatment and prevention of FHV-1
                                                                                                                                                                                                                                                   Sequence of mouse V-kappa showing the sequences of recombinant anti-FHV-1 antibody CDRs 1, 2 and 3.
                                                                                                                                                                                                                                                                           Feline herpes virus; FHV-1; monoclonal antibody; CDR; complementarity determining region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tokiyoshi
AAQ64167 standard; cDNA to mRNA; 381 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 18-19; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
1..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maeda H, Nishiyama K,
                                                                                                                                                                                                                                                                                                                                              /*tag- b
/label- MKL104
385.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERO THERAPEUTIC
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/label= MJK124
                                                                                                                                               GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAGA ) CHEMO
                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                            WO9412661-A
                                                                                                                                                                                                                                    29-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection
                                                                                                                                                                                                                     AAQ64167;
                                                                                                                                                                                                                                                                          Feline
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                                                               of
                                                                                                                                                                                                                                                                                                   CITTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACAGGTATCAACAAAAGGCCT 120
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                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                            1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACGTTCGGAGGG
and fragments of VH and VL CDR1, CDR2 and CDR3. The antbodies are used in the detection, treatment and prevention of FHV-1. The sequences of the CDRs in the VH of the recombinant anti-FHV-1 antibody are given in AAR$4092. The sequences of the CDRs in the V the recombinant anti-FHV-1 antibody are given in AAR$4093. These C
                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                    Length 381;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.
                                                                                                                                         86 G; 103 T; 0 other;
                                                                                                                                                                                                  Score 248; DB 15;
Pred. No. 1.2e-68;
                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                  77.3%;
85.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0310252.
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                                                                                                                                         Sequence 381 BP; 94 A; 98
                                                                                                                                                                                                                                         Conservative
                                                                                                  sequences are claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selick HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-190856/19.
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6180370-B1
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28-SEP-1990;
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98WO-US04987

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12-MAR-1998;
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                                                                                                 The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections. CMV virus infections and myeloid leukaemia. THe present sequence is an antibody cDNA used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                             121 ctttcctgcagggccagccaaagtattagcaacaacctacactggtatcaacaaaaatca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised antibody; monoclonal antibody; MAb; antibody engineering;
                                                                                                                                                                                                                                                                                                                                     1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTTCAGTGGCAGTGGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer: metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
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                                                                                                                                                                                                                                                                                 77.3%; Score 248; DB 22; Length 381;
85.9%; Pred. No. 1.2e-68;
1.ve 0; Mismatches 45; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                  Murine vitronectin alpha-v beta-3 receptor MAb VL cDNA.
                                                                                                                                                                                                                                             Sequence 381 BP; 97 A; 92 C; 89 G; 103 T; 0 other;
                                                                          Example 8; Fig 39; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV71798 standard; cDNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 gggaccaagctggaaataaa 380
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                                                                                                                                                                                                                                                                                  Query Match 77.3
Best Local Similarity 85.9
Matches 275; Conservative
P-PSDB; AAB69687
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This cuphs sequence codes for the light chain variable receptor (18 cee AAW84094) of the anti-human alpha v beta-3 vitronectin receptor murine monoclonal antibody D12. It was obtained from hybridoma total RNA by RT-CR using mouse kappa and N-terminal-based primers (see AAV71808-09). A heavy chain variable region clone (see AAV71797) as also been identified. D12 VH and VL show sequence similarity to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see AAW84096), respectively. Humanised VH (see AAW84097) and VL see AAW84098) were constructed by combining the framework regions of the human v region consensus sequences with complementarity determining regions of D12 (Keeping some preferred murine framework residues). The humanised antibodies are specifically reactive with the human alpha-v beta-3 protein receptor and capable of neutralising the receptor. They can be used for passive immunotherapy of a disorder mediated by the alpha-v beta-3 receptor, e.g. cardiovascular cassociated with diabetic retinopathy, atherosclerosis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoprorsis, hyperparathyroidism, Paget's disease, hypercalcenae corrections, preparathyroidism, Paget's disease, hypercalcenae corrections and diagnosis. Corrections and diagnosis, promine deficiency. They can also correct correction and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA sequence codes for the light chain variable region (VL,
                                                                                                                                                                                                                                                                                                              New anti alpha_v beta_3 vitronectin receptor antibodies - used finmunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 1.1e-66;
0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13; Page 59-60; 97pp; English.
                                                                                                                                          Taylor AH;
                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGACCAAGGTGGAAATTAA 320
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84.7%;
97US-0039609
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Best Local Similarity 84.75
Matches 271; Conservative
                                                                                                                                       Jonak ZL,
                                                                                                                                                                                                           WPI; 1999-034590/03.
                                                                                                                                                                                                                                       P-PSDB; AAW84094
                                                                                                                                       Johanson KO,
12-MAR-1997;
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Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;
           301 GGGACCAAGGTGGAAATTAA
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                               307
                                                                       AAZ35242
                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding the Fd chain of antibody MAK33 were used to transform E.coli DSM 3689 and the resulting cells grown to form inclusion bodies. After the final renaturation step an 18% yield of blologically active protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody MAK33; kappa chain; plasmid pBT111; activated antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 5238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                    Activated antibody prodn. from recombinant procaryotic cells by solubilisation under reducing conditions, then oxidative renaturation, carried out at low protein concn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                               Plasmid pBT111 encoding antibody MAK33 kappa chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                 7..663
/*tag= a
/product- kappa chain of MAK33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241.6; DB Pred. No. 3e-66; 0; Mismatches
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                          (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                  BP.
301 gggacaaacttggaaataaa 320
                                                                                                                                                                                                                                                                                                                Lenz
                                                 AAQ04654 standard; DNA; 5238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.3%;
Best Local Similarity 84.7%;
Matches 271; Conservative
                                                                                                                                                                                                                                                  88DE-3835350,
                                                                                                                                                                                                                                                                     88DE-3835350.
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; ; p; German.
                                                                                                                                                                                                                                                                                                             Buchner J,
                                                                                                                                                                                                                                                                                                                                  WPI; 1990-156813/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      see also AAQ04655
                                                                                                                                                                                                                                                  17-0CT-1988;
                                                                                                                                                                                                                                                                     17-0CT-1988;
                                                                                          01-OCT-1990
                                                                                                                                                                                                         DE3835350-A.
                                                                                                                                                                                                                             19-MAR-1990
                                                                                                                                                                                                                                                                                                             Rudolph R,
                                                                      AAQ04654;
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used for treating Verotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVTm1-1 comprising the complementarity determining regions of MuVTm1-1 and heavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain frameworks, provided that at least 1 position selected from L49, H30, H49 and H98 is occupied by the amino acid at the equivalent position of the MuVTm1-1 antibody heavy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence codes for the light chain variable region (see AX723405) of murine monoclonal antibody VTmL-1 (WMVTml-1), an antibody that specifically binds to the B subunit of verotoxin II (VT2). The invention relates to humanised antibodies against VT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vasques
                                                                                                                                                                                                                                                                                                                                                                                                                                        Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1; monoclonal antibody; light chain; mouse; humanised antibody; Escherichia coli; VTEC; Infection; haemolytic uraemic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Co MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/transl_except= (pos:184..186, aa:Lys)
                                                                                                                                                                                                                                                                                                                                                                             Mouse anti-verotoxin II antibody VTml-1 VL cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takedo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanized antibody binding to verotoxin II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haemolytic uraemic syndrome (HUS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1b; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TEIJ ) TEIJIN LTD.
(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                      AAZ35242 standard; cDNA; 381 BP.
99WO-US11179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0086570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUS; therapy; ss.
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DB 21; Length 381;

73.3%; Score 235.2;

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Claim 1; Page 440; 803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; proliferative; thrombolytic; antidfammatory; cytostatic; antibacterial; antifungal; antiviral; antidfammatory; cytostatic; antibacterial; antifungal; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonlan; antiulcer; osteopathic; neuroprotective; notropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; antima; myeloid cell déficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                               61 gatgitigigctaactcagtctccagccaccctgictgigactccaggagatagcgicagi 120
                                                                                          CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                      180
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                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                         catgagtctccaaggcttctcatcaagtctgcttcccagtccatctctgggatcccctcc
                                                                                                                                                                                                          GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAAAGGGCGACT
                                                                                                                                          121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                              AGGTTCAGTGGCAGTGGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evans C;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted expressed sequence tag SEQ ID NO:921
No. 1.2e-64;
smatches 53;
              0; Mismatches
  Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                       AAA44346 standard; cDNA; 651 BP.
                                                                                                                                                                                                                                                                                                                         361 gggaccaagctggagctgaa 380
                                                                                                                                                                                                                                                                                                  GGGACCAAGGTGGAAATTAA 320
 83.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2000 (first entry)
Best Local Similarity 83.4 Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-317938/27
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AAA AAA43926 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: Chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antidiagl; antiviral; antidiabetic; cytostatic; antipackinsonian; antipackinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 651 BP; 174 A; 166 C; 151 G; 160 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 233.6; DB 2
Pred. No. 4.8e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 11, 2001, 15:12:36
Job time: 6468 sec
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83.1%;
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Best Local Similarity
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OM nucleic - nucleic search, using sw model

October 11, 2001, 15:14:12; Search time 87.94 Seconds Run on:

(without alignments)
691.027 Million cell updates/sec

US-08-791-391A-3 321 1 GAGATTGTGCTAACTCAGTC.......GGACCAAGGTGGAAATTAAG 321 Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	& Onerv			SUMMARIES	
Score M	atch	Match Length DB	DB	Π	Description
248	77.3	381	П	US-07-634-278-82	Sequence 82, Appl
_	77.3	381	~	US-08-477-728-82	Sequence 82, Appl
248	77.3	381	Н	US-08-474-040-82	82,
248	77.3	381	-	US-08-487-200-82	Sequence 82, Appl
248	77.3	381	4	US-08-484-537-82	82,
248	77.3		~	US-08-436-463-3	m
241.6	75.3		9	5453363-1	Patent No. 5453363
	70.8	321	7	US-08-232-081B-35	Sequence 35, Appl
224	8.69		~	US-08-232-081B-36	36,
224	69.8		7	US-08-737-560A-13	13,
224	69.8	363	7	US-08-737-560A-8	8, 4
	67.3	322	~	US-08-476-176B-3	'n
216	67.3		~	US-08-127-721A-3	'n
	67.3	322	m	US-08-485-246A-3	'n
206.4	64.3	321	7	US-08-232-081B-39	Sequence 39, Appl
	63.4	318	-4	US-08-326-362-3	'n
201.2	62.7	318	7	US-08-800-198-3	3
201.2	62.7	318	٣	US-09-296-595-3	'n
201.2	62.7	720	~	US-08-800-198-7	Sequence 7, Appli
201.2	62.7		ო	US-09-296-595-7	7,
200	62.3		7	US-07-956-399-1	7,
	61.1		~	US-08-653-402B-7	Sequence 7, Appli
193.6	60.3		~	US-08-192-102-2	7
193.6	60.3			US-08-324-799-2	7
193.6	60.3		~	US-08-192-861A-2	7
	60.3	717	~	US-07-956-399-3	Sequence 3, Appli
	58.4	812	7	US-08-053-131-178	178

Sequence 178, App Sequence 41, Appl Sequence 180, App Sequence 180, Appl Sequence 19, Appl Sequence 201, Appl Sequence 9, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7	Sequence 7, Appir Sequence 216, App
US-08-096-762-178 US-09-042-353-41 US-08-053-131-180 US-08-09-762-180 US-09-042-353-43 US-09-042-353-43 US-09-042-353-43 US-09-042-353-43 US-09-042-353-43 US-08-127-721A-9 US-08-127-721A-9 US-08-137-721A-9 US-08-486-753-5 US-09-04-1889-10 US-08-486-753-5 US-08-486-753-5 US-08-486-753-5 US-08-486-753-7 US-08-486-753-7 US-08-486-753-7 US-08-486-753-7	US-09-240-274-216
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Fatent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: COELINGH, Wailliam P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SENEIDER, Wailliam P.
APPLICANT: SELICEK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lyton Avenue
CITY: Palo Alto
CITY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT AFFICATION DATA:
CURRENT AFFICATION NUMBER:
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAMME: SMITCH, WILLIAM
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
                                   Sequence 82, Application US/07634278 Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SED ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94301
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us 07/290,975

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ADDRESSEE:
                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-477-728-82
                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-474-040-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                              1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAGGGCGACT
                                                                                                                                                                                                                                                                              181 CATGAGTCTCCAAGGCTTCTCAAGTATGCTTCCCAGTCCATCTCTGGGATCCCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                            AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Embarcadero Center, 8th Floor CITY: Palo Alto
STATE: California
                                                                                                                                77.3%; Score 248; DB 1;
85.9%; Pred. No. 2.9e-70;
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
* APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/477,728 FILING DATE: 07-JUN-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 77.3
Best Local Similarity 85.9
Matches 275; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                             ; NAME/KEY:
; LOCATION:
US-07-634-278-82
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61 GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
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APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: HIPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 248; DB 1;
Pred. No. 2.9e-70;
); Mismatches 45
                                                                                                11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 82, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION:
                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.3%; Sc
ilarity 85.9%; Pr
Conservative 0;
                                                NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GGGACCAAGCTGGAAATAAA 380
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FILING DATE: 28-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                      linear
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Matches 275; Conserv
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CTTTCCTGCCAGGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
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Pred. No. 2.9e-70;
0; Mismatches 45; Indels
                                                                                  APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
UNDRER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
RILING DATE: 7-JUN-1995
                                                                                                                                                                        Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11823-002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-5EP-1990
PRIOR APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223

REEFERENDE/DOCKET NUMBER: 30,223

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 11823-00261

REGISTRATION NUMBER: 30,223

REFERENDE/DOCKET NUMBER: 11823-00261
                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 77.3%;
Best Local Similarity 85.9%;
Matches 275; Conservative (
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 381 base pairs
nucleic acid
3DNESS: single
                                                                                                                                                                                        STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..381
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                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-487-200-82
                                          APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Indels
                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentun Release #1.0, Version #1.25
SOFTWARRY APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 248; DB 1;
Pred. No. 2.9e-70;
0; Mismatches 45;
                                                                                                                                                           APPLICATION UNBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 38-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 38-DEC-1988
APPLICATION NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGGACCAAGCTGGAAATAAA 380
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGACCAAGGTGGAAATTAA 320
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85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.3
Best Local Similarity 85.9
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-08-474-040-82
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Gaps

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GENERAL INFORMATION:
APPLICANT: KIMACHI, KAZUHİKO
APPLICANT: MAEDA, HILOAKİ
APPLICANT: MAEDA, HILOAKİ
APPLICANT: TOKIYOSHI, SACHİO
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NÜMBER OF SEQUENCES: 21
                                                                                                                                            61 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                       CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAGGCCT 120
                                                                                                                                                                                                                                                                               AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT 240
                                                                                                                                                                                                                                                                                                                                                               241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGGTTCGGAGGG 300
                                       1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                      GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
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45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET 419 Seventh Street, N.W., Suite 400 STATE: D.C.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIMACHI=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08436463 Patent No. 5760185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 424 base pairs
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
Matches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-436-463-3
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241 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
                                                          241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 381;
                                                                                                                                                                                                                                                                                                                 APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold B.
APPLICANT: SELICK, Harold B.
APPLICANT: SELICK, HAROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 248; DB 4;
Pred. No. 2.9e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634.278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590.274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310.252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290.975
FILING DATE: 28-DEC-1988
ATTORNEY/ACENT INFORMATION:
NAME: SMITCH, William M REGISTRATION NUMBER: 30.223
REFERENCE/DOCKET NUMBER: 11823-00266
TELECOMMUTCATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        Sequence 82, Application US/08484537 Patent No. 6180370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOWNSEND AND TOWNSEND AND CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                     GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                        361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.3%;
85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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Best Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                     US-08-484-537-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.2e-63;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747
CITY: FALLS CHURCH STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.8%; Score 227.2; Best Local Similarity 81.9%; Pred. No. 1.2e Matches 262; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/232,081B
                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEXUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        ; Sequence 35, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTORNEY TRORMATION:
ATTORNEY AGENT IRFORMATION:
NAME: SYENSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFRENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8060
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                            307 gggaccaagctggagctgaa 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 321 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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                                                                                                                                                                                                                                                      US-08-232-081B-35
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                                                                                                                                                                                             83 GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGAGAGATAGCGTCAGT 142
                                                                                                                                                                                                                                                    CTTTCCTGCCAGGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                          143 CTTTCCTGCAGGCCAGCCAAAGTATTAGCAACAACCTACACTGGTATCAACAAAAATCA 202
                                                                                                                                                                                                                                                                                                                               121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                     121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTTTCCTGCCAGGCCAAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                        Gaps
                                                                                                                                                                          1 GAGATTGTGCTAACTCCAGTCTCCAGCCACCCTGTCTCTCAGCCCCAGGAAAGGGCGACT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
ING AFTER GENETIC EXPRESSION IN PROKARYOTES
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/206,044
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 942,370
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 98,500
FILING DATE: 23-MAR-1990
APPLICATION NUMBER: 76,207
FILING DATE: 23-MAR-1996
                                                                                                 DB 1; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                    Indels
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Pred. No. 8.7e-68;
0; Mismatches 49;
                                                                                                                                    45;
                                                                                             Score 248; DB 1
Pred. No. 3e-70;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 GGGACCAAGCTGGAGCTGAA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.3%;
                                                                                             77.3%;
85.9%;
                                                                                             Query Match 77.3
Best Local Similarity 85.9
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 84.7
Matches 271; Conservative
                23..403
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5238
NAME/KEY:
                  LOCATION:
                                    US-08-436-463-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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181 AGGTTTAGTGGCAGTGGATCAGGGACAGATTTTACTCTTACATCTCCCAGGCTGGAGCCA 240
                                                                                      Gaps
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                                                                241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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; Patent No. 5928893
; GENERAL INFORMATION:
    APPLICANT: KANG, Chang-Yuil
    APPLICANT: KIM, Joong-Gon
    TITLE OF INVENTION: MONCLONAL ANTIBODY SPECIFIC FOR HUMAN
    TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
    TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: Kwanak-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Republic of Korea
ZIP: 135-110
ZIP: READBLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 224; DB 2; Pred. No. 1.2e-62; Pred. No. 1.2e-62; Pred. Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/737,560A FILING DATE: 13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KR 95-8176
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                              301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                        GGGACCAAGGTCGAGATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Republic of Korea ZIP: 151-057
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81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.8°
Best Local Similarity 81.2°
Matches 260; Conservative
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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); OTHER INFORMATION:
US-08-737-560A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13
CLASSIFICATION:
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US-08-737-560A-13
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241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                    CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: FALLS CHORCH
STATE: VA
COUNTRY: VSA
ZUE: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILLING DATE:
                                                                                                                                                                                                                                                                               Sequence 36, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: MACATANI, TOMOYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: WIJDENES, JOHN
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SYENSON, LECONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 36:
SEGUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
                                                                                                                                            301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                               301 GGGACCAAGGTCGAGATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 260; Conserv
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STRANDEDNESS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
APPLICANT: KANG, Chang-Yuil
APPLICANT: KIM, Joong-Gon
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: Republic of Korea
21P: 151-057
ADDRESSE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: Kwanak-gu
CITY: Seoul
STATE: Seoul
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MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
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APPLICATION NUMBER: US/08/737,560A
FILING DATE: 13.nov-1996
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-8176
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08737560A Patent No. 5928893 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               301 GGCACCAAGCTGGAAATCAA 320
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Word Perfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC,
OPERATING SYSTEM:
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US-08-737-560A-8
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70 to 102 bp hypervariable region CDR1
148 to 168 bp hypervariable region CDR2
265 to 291 bp hypervariable region CDR3
325 to 363 bp 484-1-1 light chain constant region
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                                                                                                                                                                                                                                  Length 363;
                                                                                                                                                                                                                                  69.8%; Score 224; DB 2; Length 36
81.2%; Pred. No. 1.3e-62;
ive 0; Mismatches 60; Indels
  1 to 324 bp 4B4-1-1 light chain
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APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08476176B
Patent No. 5958708
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                     CTHER INFORMATION:
CTHER INFORMATION:
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CITY: East Hanover
STATE: New Jersey
OTHER INFORMATION:
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Best Local Similarity
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ZIP: 07936-1080
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US-08-476-176B-3
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GAAGATATTGCAGATTATTACTGTCAACAAAGTGATAGCTGGCCAACCACCACGTTCGGAGGG 300
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Partent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Scaldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: No. 6066718artis Patent and Trademark Department STREET: 59 Route 10 CITY: East Hanover STATE: New Jersey STATE: New Jersey 2CUNTRY: USA ZIP: 07936-1080
                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 216; DB 2; Length 322; 79.7%; Pred. No. 4.5e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Indels
                                                                                                                                                                                                                                                                                                          /product- "light chain variable domain of murine antibody TES-C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
NAME: NO. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TELNOTH: 322 base pairs
TENTHE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GGGACCAAGCTGGAGATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 79.7
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                       LOCATION: 1.321
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-127-721A-3
                                                                                                                                                                                                                                                                                                                                               US-08-476-176B-3
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121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 6072035
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 67.3%; Score 216; DB 3; Length 322; Best Local Similarity 79.7%; Pred. No. 4.5e-60; Matches 255; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product- "light chain variable domain of murine antibody TES-C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
                                                                                                                                                                           ATTORNEY/AGENY INCOMMENTATION

NAME: NO. 606671884, Henry P.

REGISTRATION NUMBER: 31,200

REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 277-5110

TELEFAX: (908) 277-5110

TELEFAX: (908) 277-4306

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
27-SEPTEMBER-1993
1: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
COCATION: 1..321
OTHER INFORMATION:
CTHER INFORMATION:
US-08-127-721A-3
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                                                       CLASSIFICATION:
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Search completed: October 11, 2001, 15:14:14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTTTCCTGCCAGGCCAGGCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
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Best Local Similarity 79.7%; Pred. No. 4.5e-60;
Matches 255; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "light chain variable domain of murine antibody TES-C21"
                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/POCKET NUMBER: 4.19276/A/P2/CIP
TELECOMMUNICATION:
                                 ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-232-081B-39

Sequence 39, Application US/08232081B

Patent No. 5886152

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: , OTHER INFORMATION: , ; OTHER INFORMATION: c US-08-485-246A-3
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                    FILING DATE:
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121 GGTCAAGCCCCAAGGCTTCTCATCATCATATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGCTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTGAGTCCAGGAGAAAGAGTCAGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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APPLICANT: GOMI, HIDEVUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: WIJDENES, JOHN
APPLICANT: WIJDENES, JOHN
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Catentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/08/232,081B FILING DATE: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 206.4; DB 2;
Pred. No. 5.2e-57;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELEPONNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
                                                                                                                                                                                              CITY: FALLS ......
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
~~WEDIUM TYPE: TEM PC compatible
~~WEDIUM TYPE: TEM PC COMPATIBLE
~~WEDOS/MS-DY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 ĠGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.3%;
Best Local Similarity 77.8%;
Matches 249; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-232-081B-39
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Job time: 5001 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:02:35; Search time 31.63 Seconds

(without alignments)
257.688 Million cell updates/sec

Title: US-08-791-391A-4

Perfect score: 561
Sequence: 1 EIVLTQSPATLSLSPGERAT......CQQSGSWPHTFGGGTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 219241 seqs, 76174552 residues
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: PIR_68:*
1: pir1:*
2: pir2:*
3: pir2:*
4: pir4:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query Match	Length	DB	QI .	Description
1	469	83.6	144	~	PL0106	Iq kappa chain pre
7	459	\vdash	111	7	S23628	kappa chain
m	457	81.5	128	7	A56701	kappa chain V
4	456		128	~	S40379	chain V-
2	453	80.7	107	~	B45722	u
9	451.5	ö	114	~	S54905	Iq kappa chain V r
7	450	80.2	108	7	G44151	Iq kappa chain V r
œ	448	79.9	123	7	S35479	kappa chain pr
თ	447	79.7	107	7	A45722	i-qlycoprote
10	446	79.5	106	~	PC4282	Ig kappa chain (an
11	443	79.0	117	7	S40362	
12	442	78.8	106	~	PL0267	kappa
13	442	78.8	125	~	S40344	Iq kappa chain V-J
14	439.5	78.3	109	~	A30608	kappa
15	439		129	7	S29627	
16	437	٠	128	~	S40345	
17	436	•	101	~	S34005	
18	433.5	77.3	129	7	A32274	
19	432.5		108	7	B30608	kappa
20	431.5		109	7	G30607	kappa
21	430.5	ė.	109	-	K3HUTI	kappa
22	430	9	107	~	S57444	
23	429.5	9.9/	109	ď	D30601	Iq kappa chain V-I
24		9.9/	109	7	C30601	
25		•	109	~	H30601	
56	42	9	128	7	S40343	kappa
27	427.5	76.2	109	Н	K3HUSI	Ig kappa chain V-I
28	26.	٠	109	7	G30601	kappa
29		76.0	109	~	B30601	

Iq kappa chain V r	Iq kappa chain pre	Iq kappa chain NIG	Ig kappa chain pre	Iq kappa chain v-I	Iq kappa chain V r	anti-Sm antibody V	Iq kappa chain v r	Ig kappa chain V r	Ig kappa chain V-I	Ig kappa chain V-I	Ig kappa chain pre	Iq kappa chain v r	Ig kappa chain V r	Ig kappa chain pre	Ig kappa chain v r
320636	КЗНИНА	JE0244	A26471	C30608	S20635	S49532	C30502	PH0963	F30607	K3HUWL	K3HUHI	S26346	S19975	PN0445	B43413
O)															
7	Н	7	7	7	7	7	7	7	7	-	٢	7	7	7	~
128 2 8	129 1	215 2	138 2	108 2	110 2	129 2	108 2	109 2	109 2	109 1	129 1	102 2	103 2	128 2	104 2
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76.0	. 0.92	75.8	75.8	75.7	75.5	75.5	75.4		75.3	75.1	75.1	75.0	74.9	74.9	74.7

ALIGNMENTS

219241

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

```
Ig kappa chain precursor V-J-C region (LS1) - numan (LLSymeries)

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PL0106
R;Silberstein, L.E.: Litwin, S.; Carmack, C.E.
J. Exp. Mad. 169, 163-11643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma s A;Reference number: PL0106; MUID:89235583
A;Accession: PL0106
A;Residues: 1-144 <SILO
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-115/Domain: signal sequence #status predicted <SIG>F;31-115/Domain: omplementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region (fragment) <CRE>
F;128-144/Domain: C region (fragment) <CRE>
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C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: 13-3mn-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C; Accession: S23628

R; Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A. J. Exp. Med. 175, 831-842, 1992

A; Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro A; Reference number: S23623; MUID:92156804

A; Accession: S23628

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-111 < OLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.6%; Score 469; DB 2; Length 144;
85.0%; Pred. No. 1.9e-34;
tive 6; Mismatches 10; Indels
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Best Local Similarity 85.0
Matches 91; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A;Reference number: A45722; MUID:93100833
A;Accession: B45722
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A; Description: Cloning and sequencing of cDNA coding for the variable domains of a hu
A; Reference number: $54905
A; Accession: $54905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33)
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C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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                                                                                                                                                                  1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X82934; NID:g809554; PIDN:CAA58108.1; ISCS-Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin call E;16-90/Pomanin: immunoglobulin homology <IMM>
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Pred. No. 5.3e-33;
......hes 9;
                                           13;
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76.6%; Pred. No. 3.7e-33;
ive 17; Mismatches 8;
           81.3%; Pred. No. 2.4e-33;
live 7; Mismatches 13
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F;16-90/Domain: immunoglobulin homology <IMM>
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                                               87; Conservative
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       Best Local Similarity
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Matches 82; Conserv
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A;Molecule type: mRNA
A;Residues: 1-114 <ESP>
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C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: 19-0ct-1995 #sequence_revision 19-oct-1995 #text_change 21-Jan-2000
C. Species: A56701
B. Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
J. Biol. Chem. 270, 12457-12465, 1995
J. Rickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
A. Title: Human and mouse monoclonal antibodies to blood group A substance, which are na A. Reference number: A56701
A. Reference number: A56701
A. Reference number: A56701
A. Molecule type: mRNA
A. Residues: 1-128
A. NIC>
A. Cross-references: GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:g762824
C. Superfamily: Immunoglobulin V region; immunoglobulin homology
C. Superfamily: Immunoglobulin homology <IMM>
F:36-110/Domain: immunoglobulin homology <IMM>
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A;Cross-references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <a href="https://document.com/restrances/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burnes/burne
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                                                                                                                                                                                                                                     Score 459; DB 2;
Pred. No. 1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.5%; Score 457; DB 2; 82.2%; Pred. No. 2e-33;
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                                                                                                                                                                                                                                                                                                            7; Mismatches
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                                                                                                                                                                                                                                     81.8%;
83.2%;
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Best Local Similarity 82.2°
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                89; Conservative
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 89; Conserv
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Ig Kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment) C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C; Accession: PG4282; PC4284
R; Suzuki, H; Takemura, H; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A; Title: Molecular cloning of anti-ss-A/Ro 60-kba peptide fab fragments from infiltra A; Reference number: PC4279; MUID:97236289
                                                                                                                                                                                                        Gispedies: Mus musculus (house mouse)
Cispedies: Mus Mission (house)
J. Virol. 67, 489-496, 1993
A. File: Neutralizing monoclonal antibodies that distinguish three antigenic sites of A. Reference number: A45722; MuID:93100833
A. Reference number: A45722; MuID:93100833
A. Recession: A45722
A. Status: preliminary: not compared with conceptual translation
A. Residues: 1-107 <SIM
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                                                                                                                                                                                      anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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       RFSGSGSGTDFTLSINSVETEDFGMYFCQQSNSWPHTFGSGTKLEIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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74.8%; Pred. No. 1.2e-32;
iive 18; Mismatches 9;
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; Pred. No. 1.5e-32;
10; Mismatches 10;
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Best Local Similarity 81.0%;
Matches 85; Conservative 1
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A; Molecule type: protein
A; Residues: 1-106 <SU2>
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Best Local Sim:
Matches 80;
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Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
Proc. Natl. Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:9228746
A;Recession: G44151
A;Reference: G44151
A;Relecule type: mRNA
A;Residues: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-108 < ZEB>
A;Cross-references: GB:M88317; NID:9183968; PIDN:AAA35975.1; PID:9183969
A;Cross-references: GB:M88317; NID:9183968; PIDN:AAA35975.1; PID:9183969
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
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A. Reference number: $35479; MUD:92375706
A. Status: nucleic acid sequence not shown
A. Status: nucleic acid sequence not shown
A. Status: nucleic acid sequence not shown
A. Residues: 1-123 <TAK>
A. Residues: 1-123 <TAK>
A. Residues: 1-123 <TAK>
A. Residues: 1-123 <TAK>
A. Charastreferences: EMBL: M93959; NID:g197572; PIDN: AAA39079.1; PID:g554148
C. Genetics:
A. Map position: 6
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Superfamily: immunoglobulin #status predicted <MAT>
F:1-12, Domain: signal sequence (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                              C.Species: Homo sapiens (man)
C.Date: 27-Jun 1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain precursor V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Musr-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S;347;9
R;Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
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                                        61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPH-TFGGGTKVEIK 107
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Pred. No. 6.8e-33;
8; Mismatches 10
                                                                                                                                                                                                                                                Ig kappa chain V region (JM-10) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.2%;
82.7%;
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Best Local Similarity
Matches 86; Conserv
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Local Sim.
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C;Species: Homo sapiens (man)
C;Species: Bomo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: A30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
J. Immunol. 147, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A;Reference number: A30601; MUID:89215279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: More Sallo; S29627
C.Species: Natlo: More Sallo; S29627
Nucleic Acids Res. 21, 2921-2929, 1993
A.Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains A.Reference number: S34110; MUID: 93324379
A.Recession: S34110
C.Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C.Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C.Accession: S40344
R.K.Hain, R., Jaenchen, R.; Zachau, H.G.
B.r. J. Immunol. 23, 3248-3271, 1993
A.; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Accession: S40312; MUID:94080891
A; Accession: S4034; translation not shown
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                               A; Residues: 1-125 <KLE>
A; Cross-references: EMBL.X72454; NID:g441376; PIDN:CAA51122.1; PID:g441377
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 439.5; DB 2;
Pred. No. 5.7e-32;
7; Mismatches 12;
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3.9e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 442; DB Pred. No. 3.9e-5; Mismatches
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ilarity 81.5%;
Conservative 7
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nilarity 81.9%;
Conservative
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A;Molecule type: protein
A;Residues: 1-109 <GON>
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Best Local Similarity
Matches 86; Conserv
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nes 88; Conserv
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C; Species: Was musculus (house mouse)
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C; Accession: PLO267
R; Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, P. T. Exp. Med. 171, 26-297, 1990
A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A; Reference number: PLO231; MUID:90111618
A; Accession: PLO267
A; Molecule type: mRNA
A; Residues: 1-106 ASHLD
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <IMM>F; 16-39/Region: framework I munoglobulin fr. F: 16-34/Region: complementarity-determining 1
F; 15-44/Region: complementarity-determining 2
F; 50-56/Region: framework 2
F; 50-56/Region: framework 4
F; 98-106/Region: framework 4
F; 98-106/Region: framework 4
                      Ly Arrera Library 1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C; Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C; Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C; Date: 05-May-1996 #text_change 21-Jan-2000 C; Date: 06-Mar-1994 #sequence_revision Expression: 8.348-3271, 1993 A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: 840312; MUD:9408091 A; Reference number: 840312; MUD:9408091 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-117 < KLE> A; Cross-references: EMBL:X72472; NID:9441412; PID:9441413 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 26-100/Domain: immunoglobulin homology < NIMM>
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
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Pred. No. 3.4e-32;
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S40344
Ig kappa chaiz V-J region - human
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Best Local Similarity 75.5%
Matches 80; Conservative
         Ig kappa chain - human
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A; Molecule type: mRNA
A; Residues: 1-129 <WA2>
A; Cross-references: EMBL:217330; NID:938511; FIDN:CAA78978.1; FID:938512
A; Cross-references: EMBL:217330; NID:938511; FIDN:CAA78978.1; FID:938512
A; Mote: human sequences cloned and sequenced prior to expression in mouse myeloma cells A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C; Genetics:
A; Introns: 17/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 36-110/Domain: immunoglobulin homology < IMM>
A; Status: nucleic acid sequence not shown; translation not shown
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homo sapien

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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A BEQUENCE.

RX MEDLINE-72188439; PubMed-5027703;

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RT. "Rule of antibody structure. The primary structure of a monoclonal

RT II munoglobulin L-chain of Kappar type, subgroup 3 (Bence-Jones protein

RT TI). IV. The complete amino acid sequence and its significance for

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RT TI). IV. The Complete amino acid sequence and its significance for

RL HOPPE-Seyler's Z. Physiol. Cham. 353:189-208(1972).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR, A01895; K3HUTI.

DR PEAM; PE00047; 19; 1.

DR PEAM; PE00047; 19; 1.

RW Immunoglobulin V region; Bence-Jones protein.

-- TENTERINEOUS THE C REGION OF THIS INV (3) MARKER.

-- TENTERINEOUS THIS IS A BENCE-JONES PROTEIN.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION SIE.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P01603
P01674
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P01601
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Best Local Similarity 80.6%; Pred. No. 2.6e-37;
Matches 87; Conservative 5; Mismatches 15
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION TI.
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                                 KV3V_MOUSE
KV3S_MOUSE
KV1D_HUMAN
KV1B_HUMAN
KV1R_HUMAN
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KV1O_HUMAN
KV1S_HUMAN
KV3N_MOUSE
            KV3I_MOUSE
KV1K_HUMAN
  KV30_MOUSE
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P01599
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                             93435 segs, 34255486 residues
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KV1M_HUMAN
KV1H_HUMAN
                                                                               October 11, 2001, 12:08:43
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KV3L_HUMAN
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KV3M_HUMAN
KV3H_HUMAN
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KV3F_HUMAN
KV3K_HUMAN
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KV5I_MOUSE
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KV1E_HUMAN
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KV1N_HUMAN
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Listing first 45 summaries
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Best Local Similarity
Matches 86; Conserv
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P01623;
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KV3M_HUMAN
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PIR; A01992; K3HUSI.
HSEP; P01789; ZMCP.
InterPro, IPR003006; -.
                                                                                                 Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idlotypically cross-reactive human IgM anti-gamma-globulins of the Wa
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Inplications for etiology and immunotherapy.";

J. Exp. Med. 167:440-652(1988).

-I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
BY SIMILARITY.
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRFSGSGGTDFTLTISRLEPDDFAVYCQQYGSSPQTFGQGSKVEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                      109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
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Pred. No. 5.2e-37;
7; Mismatches 14;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-UL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
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FRAMEWORK 1
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Immunoglobulin V region; Signal.
                                                                                                                                                                                 Biochemistry 20:5816-5822(1981)
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79.68;
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Pfam; PF00047; 19; 1.
Immunoglobulin V region.
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HSSP; P01789; ZMCP.
InterPro; IPR003006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from tidiotypically cross-reactive human IgM anti-gamma-globulins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                             Indels
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14073 MW; D3C55292772774D0 CRC64;
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Pred. No. 2.1e-36;
6; Mismatches 15;
                                                           Score 426.5; DB 1;
Pred. No. 8e-37;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION WOL.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-UL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION HIC PRECURSOR.
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milarity 79.6%;
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SEQUENCE FROM N.A.
MEDLINE SEQUENCE FROM N.A.
MEDLINE F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
JITIK F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor
"Cloning and sequence determination of a human rheumatoid factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
                                       MEDITARE 88171307; PubMed-3127527;
Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;
Ripps T.J. Tomhave E., Chen P.P., Carson D.A.;
Antoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOCLOBULIN MAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 129;
                                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           14070 MW; 7395528EA2BB74D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 421.5; DB 1
Pred. No. 2.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AA.
                                                                                                                                                                                                                                                                                                                                                                              JK1 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                            PIR; PL0021; K3HUHI.
HSSP, P01789; 2MCP.
InterPro; IPR003006; -.
Pfam; PP00047; ig; 1.
Immunoglobulin V region; Signal.
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109
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110
119
43
129
129 AA;
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Best Local Similarity
Matches 86; Conserv
                          SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                   LEUKEMIA.
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P04207;
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KV3H_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pech M., Zachau H.G.; "Immorphysis are interdigitated "Immunosjlobulin genes"; within the VK locus." Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 129;
                                                                                                                                 IG KAPPA CHAIN V-III REGION CLL.
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                                                                                                                                                                       COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
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COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSW-PHTFGGGTKVEIK 107
                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                        5C13B411BE60CC14 CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                   74.4%; Score 417.5; DB 1
75.9%; Pred. No. 6.6e-36;
                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                              FRAMEWORK 3.
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                                                                                                                                                       FRAMEWORK 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=85087932; PubMed=6440122;
PIR; A01898; K3HUCL.
HSSP; P01789; ZMCP.
InterPro.; IPRO03006; -.
Pfam; PF0047; ig; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                        14275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.4%;
Best Local Similarity 75.9%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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InterPro, IPR003006; -.
Pfam; PF00047; 19; 1.
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P04433;
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SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           128
128 AA;
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Best Local Similarity
          NCBI_TaxID=9606;
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P01619;
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDIINE=76276460; PubMed-60899;
Klapper D.G., Capra J.D.;
The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Paris) 1270:261-271(1976).
I Immunol. (Paris) 1270:261-271(1976).
GLOBULIN ACTIVITY.
PIR; A01897; K3HUPM.
                                                                                  Gaps
                                                                                                    1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIVLTQSPATLSLSPGERATLSCQASQSISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                            Length 115;
 COMPLEMENTARITY - DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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115 COMPLEMENTARITY-DETERMINI
108 BY SIMILARITY.
115
12575 MW; 2DE47CDA3A17D555 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                         Score 412; DB 1; Le
Pred. No. 2.1e-35;
7: Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%; Score 409.5; DB 1; larity 75.0%; Pred. No. 3.6e-35; Conservative 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G'KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
HOMO sapiens (Human).
                                                                                                                                                                                                                 KV3F_HUMAN STANDARD; PRT; 109 AA. P01624; 21-JUL-1986 (Rel. 01, Created) 1-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) IG KAPPA CHAIN V-III REGION POM.
                                                                                                                                                       61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWP 95
                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                          Query Match 73.4%;
Best Local Similarity 83.2%;
Matches 79; Conservative 7
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Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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P06311;
DOMAIN
DISULFID
NON_TER
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SEQUENCE
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KV3F_HUMAN
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"The basic sequences of immunoglobulin kappa chains: sequence studies of Benero Jones proteins Rad, Fr4 and B6.";
of Benero Jones proteins Rad, Fr4 and B6.";
FEBS Lett. 2:301-304(1969).
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01891; X3HUB6.
HSSP; P01789; 2MCP.
InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-III REGION IARC/BL41.
SEQUENCE FROM N.A.

BEDLINE-BROGATS, PubMed-2997711;

Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;

"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 72.9%; Score 409; DB 1; Length 128; 1 Similarity 74.8%; Pred. No. 4.8e-35; 80; Conservative 11; Mismatches 16; Indels
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14070 MW; CC8957F0FE3B9012 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA
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                                                                                                                                             Nucleic Acids Res. 13:6499-6513(1985)
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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128
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Scand. J. Immunol. 5:677-684(1976).
-!- MISCELLANDOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIVLTOSPATLSLSPGERATLSCQASOSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
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1 DIQMIQSPSSLSVSVGDRVIITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-71032830; PubMed-4097974;
Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                       "Complete amino acid sequence of the variable domains of IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 379; DB 1; Length 10; Pred. No. 4.5e-32; 21; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                    23 FRAMEWORK 1.
34 COMPLEMENTARITY-DETERMINING
49 FRAMEWORK 2.
56 COMPLEMENTARITY-DETERMINING
88 FRAMEWORK 3.
97 COMPLEMENTARITY-DETERMINING
107 FRAMEWORK 4.
88 B SIMILARITY.
108
A; 11834 MW; 739993A95431434A CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-I REGION HAU.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                      MEDLINE=77038198; PubMed=824717; Capra J.D., Klapper D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.6%;
63.6%;
                                                                                                                                                                                                                              GLOBULIN ACTIVITY.
PIR; A01871; K1HULY.
HSSP; P01607; 1REI.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
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Best Local Similarity
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P01600;
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KV1H_HUMAN
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Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

Newmarcoid factor of the Wa idiotypic group, in part predicted by its reactivity with antipeptide antibodies.";

Mol. Immunol. 23:239-244(1986).

PIR; A01893; X3HGG.

HSSP; P01789; ZMCP.

InterPro; IPR003066; -.

Pfam; PF00047; ig; 1.

Immunoglobulin V region.
                                                                                                                                              Gaps
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                                                                                                                                                                           1 EIVLTQSPATLSLSPGERATLSCQASQSIS-NHLHWYQQRPGQAPRLLIKYRSQSISGIP 59
                                                                                                                                                                                               1 EIVLTQSPATLSLSPGERATLSCQAS-QSISNHLHWYQQRPGQAPRLLIKYRSQSISGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BIVLTQSPGTLSLSPGERATLSCRAALLSSRGYLAWYQQKPGQAPRLLMYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVIM_HUMAN STANDARD; PRT; 108 AA.
P01605;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 AAPPA CHAIN V-I REGION LAY.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
16 KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
17 EUKATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Eutherenses; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                           Length 108;
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                                                                                                                                                                                                                                                60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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                                                                                                                                            Indels
                                                    8BC14FF07A419E3D CRC64;
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                                                                                                        72.3%; Score 405.5; DB 1;
73.1%; Pred. No. 9.1e-35;
Live 12; Mismatches 16;
Immunoglobulin V region; Bence-Jones protein.
DISULFID 23 89 BY SIMILARITY.
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                                                      108 AA; 11635 MW;
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Best Local Similarity 73.1%
Matches 79; Conservative
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Matches 82; Conserv
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P04206;
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MEDLINE-79012520; PubMed-99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
                                                                                                                                           Gaps
                                                                                                                                                                              Gaps
                                                                                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (PC 3741).
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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            COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
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COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
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                                 COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
                                                                                                                  Length 108;
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                                                                                                                   Score 372; DB 1;
Pred. No. 2.3e-31;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
                                                                                                         66.3%; Sco...
65.4%; Pred. No. ...
... 20; Mismatches
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Best Local Similarity 65.4°
-heq 70; Conservative
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108 AA;
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P01660;
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SECUENCE FROM N.A.

MEDLINE-81220975; PubMed=6264318;
Pech M., Hochtl J., Schnell H., Zachau H.G.;
Pech M., Hochtl J., Schnell H., Zachau H.G.;
Poth M., Hochtl J., Schnell H., Zachau H.G.;
Poth Sequences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:666-670(1981).
I- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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56 SGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
               60 SGIPARFSGSGSRIDFILIINPVEADDVATYYCQQSNEDPYTFGGGTKLEIK 111
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Pred. No. 3.2e-31;
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                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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72.6%;
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                                                                                                                                                                                     Mus musculus
                                                                                                 KV51_MOUSE
P01642;
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KV5I_MOUSE
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2000 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPH-TFGGGTKVEIK 107
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09UB05
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09WTN4
077624
09UL84
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09NP29
09H5Z4
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HSSP; P01607; 1REI.
InterPro; IPR003006; -.
Interpro; IPR003596; -.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                     Best Local Similarity 78.78
Matches 85; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
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InterPro; IPR003006; -. InterPro; IPR003596; -. Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1.
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1 Similarity 80.6%;
87; Conservative
  HSSP; PU1/U9; INC...
InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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Q9UL86
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Q9UL77
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                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!* SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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MUZ., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
61 RFSGSGSGTEFTLTISSLQSEDFAIXHCQQXNSWPPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 108
108 Aa; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                      108 AA
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                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AP035031, AAD56267.1; -
HSSP; P01607; IREI
InterPro; IPR003006; -
InterPro; IPR003596; -
Ffam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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01-MAY-2000 (TIEMBLIEL: 13, Created)
01-MAY-2000 (TIEMBLIEL: 13, Last sequence update)
01-MAR-2001 (TIEMBLIEL: 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annocation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                            1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                              SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                  68.4%; Score 384; DB 4; Length 108;
69.2%; Pred. No. 1.9e-35;
ive 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                               EMBL; AF035037; AAD56273.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                           Local Similarity 69.29
nes 74; Conservative
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                                                                                                                                                                                                                  InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGV; 1.
                                                                                                                                                                                                                                                                         108
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                                                                           NCBI_TaxID=9606;
                                                                                                                                 Young D.C.;
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NON_TER
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SEQUENCE
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Q9UL79;
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
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01-MAY-2000 (TTEMBLrel. 13, Last sequence update)
01-MAR-2000 (TTEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                        Gaps
                                                                                                          1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                   0; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                     ;
0
66.1%; Score 371; DB 4; Length 108;
llarity 67.3%; Pred. No. 5.4e-34;
Conservative 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISCLQSEDFATYXCQQYYSFPPTFGQGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           108 AA
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MEDLINE-98277139; PubMed-9614934;
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Interpro; IPR003006; -. Interpro; IPR003566; -. Pfam; PF00047; ig; 1. SMART; SMO0406; IGV; 1. NON-TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                      Best Local Similarity
Matches 72; Conserv
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acety!-glucosamine anti-bodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206032; AAF69330.1; -.
InterPro; IPR003066; -.
Fram: PF00047; 19; 1.
SMART; SM00406; IGV; 1.
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Malkel S., Lido L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF206022; AAF69320.1; -.
Interbro; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                     1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                              11 LSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPARFSGSGSGTD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-WAR-2001 (TREMBLRel. 16, Last annotation update)
ANTI-WYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                             99 AA; 10939 MW; 3B25D0E784533324 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.4%; Score 333; DB 11; Best Local Similarity 61.9%; Pred. No. 8.4e-30; Matches 60; Conservative 18; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 FTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
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Q9JL74;
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09JL84;
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                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma japonicum (Blood fluke).
Eukaryota, Metazoa, Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.; "Amplification, cloning and sequence analysis of the light chain variable region gene of monoclonal anti-idiotypic antibody NP30 c
                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.4%; Score 361.5; DB 4; Length 107; 66.4%; Pred. No. 6.1e-33; Live 17; Mismatches 18; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 106;
                                                                 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                       11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11478 MW; F20F544426BAE63E CRC64;
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59.8%; Pred. No. 2.9e-30;
ive 18; Mismatches 24;
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                   SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
                                                                                                                                                                                                                         EMBL; AF035033; AAD56269.1; -HSSP; P80362; 1WTL.
InterPro; IPR003006; -InterPro; IPR003596; -Ffam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF207620; AAF19434.1;
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.4% hes 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Watch 60.2
Best Local Similarity 59.8
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA;
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Matches
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SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Sübmitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI53371; AAD40242.1;
HSSP; P01789; IMCP.
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF206038, ARF69326.1;
InterPro; IPR003596;
InterPro; IPR003596;
Pfam; PF00047; ig: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musingel.TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23922 MW; 52BA205FDE995E2A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 58.8%; Score 330; DB 11; 1 Best Local Similarity 55.1%; Pred. No. 4.4e-29; Matches 59; Conservative 25; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%; Score 325; DB 11;
62.0%; Pred. No. 6.7e-29;
iive 16; Mismatches 20;
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InterPro; IPR003006; -
InterPro; IPR003600; -
Pfam; PF00047; ig; 2.
PROSITE; PS00209; IG_MIC; UI
SMART; SM00410; IG_like; 1.
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Best Local Similarity 62.0%
Matches 62; Conservative
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214 AA;
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101 AA;
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         DDT BENEFIT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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Shinobara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                         1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                           Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB036341; BAA88633.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; -.
InterPro; IPR003596; -.
Ffam; PF00047; 19; 2.
SMART; SMO0406; IGY; 1.
SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK
                                                                                                                                               107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  59.4%; Score 333; DB 11;
58.9%; Pred. No. 9.2e-30;
tive 15; Mismatches 29;
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Best Local Similarity 57.4%; Pred. No. 3.9e-29;
Matches 62; Conservative 26; Mismatches 18;
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01-MAY-2000 (TrEMBLrel. 13,
01-WAR-2001 (TrEMBLrel. 16,
CN 8 SCFV.
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Best Local Similarity 58.99
Matches 63; Conservative
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      InterPro; IPR003596; -.
                        SMART; SM00407; 19; 1.
SMART; SM00406; IGV; 1.
NON_TER 1
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SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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Q9R1A5 Q9R1A5;

RESULT 13 Q9R1A5 ID Q9R1A5 AC Q9R1A5

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Length 101;

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The SEQUENCE FROM N.A.

RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

RA "Cloning and sequencing of the light chain fragment of variable region genes of an anti-hTNF-a monoclonal antibody.";

RT Genes of an anti-hTNF-a monoclonal antibody.";

J. Cell. Mol. Immunol. 12:21-26(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

RA Chon P., Deng J.B., Mang Z.L., Han H., Yao L.B., Su C.Z.;

RT "Construction and sequencing of the single-chain antibody gene of a RT human TNF-alpha specific monoclonal antibody.";

RI Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                            61
10 TLSLSPGERATLSCQASQSI-SNHLHWYQQRPGQAPRLLIKYRSQSISGIPARFSGSGSG 68
                                            Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI HUMAN TNF-ALPHA LICHT CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.0%; Score 314; DB 11; Length 107; 54.2%; Pred. No. 1.2e-27; tive 22; Mismatches 21; Indels
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SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF262753; AAG23804.1; -.
NON_TER
SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;
                                                                                                                                                         69 TDFTLTISSLEPEDFAVYYCQQSGSWP-HTFGGGTKVEIK 107
                                                                                                                                                                                              107 AA.
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Best Local Similarity 54.2%
Matches 58; Conservative
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Q9ERZ9
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Gaps

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4 LTQSPATLSLSPGERATLSCQASQSI-----SNHLHWYQQRPGQAPRLLIKYRSQSISG 57

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561
1 EIVLTQSPATLSLSPGERAT.......CQQSGSWPHTFGGGTKVEIK 107
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**SiDS8/gcgdata/geneseqp/AA1980.DAT:**

**SiDS8/gcgdata/geneseq_geneseqp_AA1981.DAT:**

**SiDS8/gcgdata/geneseq_geneseqp_AA1981.DAT:**

**SiDS8/gcgdata/geneseq_geneseqp_AA1981.DAT:**

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**SiDS8/gcgdata/geneseq_geneseqp_AA1991.DAT:**

**SiDS8/gcgdata/gen
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412676 segs, 60623988 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Vitaxin antibody 1	Vitaxin light chai	LM609 grafted anti	Light chain variab	Humanised VL regio	Humanised CMV5 ant	Human Wol antibody	Humanised anti-alp	Vitronectin alpha-	Kappa light chain	Kanna light chain
SUMMARIES	QI	AAW76002	AAB61360	AAW76006	AAB61364	AAR25729	AAB69678	AAB69690	AAW84098	AAW84100	AAW08946	AAWORGAR
	DB	19	22	19	22	13	22	22	20	20	18	ä
	Query Match Length DB	107	107	107	107	107	107	107	107	112	127	107
dФ	Query Match	100.0	100.0	98.9	6.86	91.3	91.3	91.3	6.06	6.06	90.4	80
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ligh	Mouse anti-verotox The variable light	riable	Light chain variab	Light chain variab	AP	Humanised antibody	Vkappa region of h	Light chain variab		scrv fragment of h	chain	chain var	antibody	Antibody LM609 lig	Ω	Jk gene product.	Humanised anti-alp	Murine monoclonal	Human Fab clone LD	Human anti-HER2/ne	Anti-Factor-IX hum	Murine CMV5 antibo	Murine CMV5 antibo	Anti-human TNF-alp	Sequence of mouse	Light chain variab	IgG	ORF 1 of 1gG light		IgG abe	n HIV-	HYH light chain.
AAW08949	AAY30205 AAY30205	AAY30203	AAR50192	AAY26982	AAR37612	AAY71240	AAY70604	AAR50187	AAY26980	AAY70605	AAR50191	AAY26981	AAW76004	AAB61362	AAY71238	AAW87456	AAW87458	AAY06380	AAB66414	AAB72884	AAW24513	AAB69677	AAB69687	AAY08599	AAR54093	AAR52033	AAR12128	AAR12129	AAR13111	AAR13018	AAB62756	AAR38601
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494	4 90 4 89	488	486	486	484	483	480	480	480	480	477	477	470	470	459	456	456	455	454	449.5	448.5	447	447	445	444	440	439	439	439	439	437.5	3
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ALIGNMENTS

AAW76002 standard; Protein; 107 AA.

AAW76002

RESULT

AAW76002;

Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis. Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 Vitaxin antibody light chain variable region protein fragment. 98WO-US01826 97US-0791391 (first entry) WPI; 1998-437472/37. N-PSDB; AAV49821. Glaser SM, Huse WD; (IXSY-) IXSYS INC. WO9833919-A2. 30-JAN-1997; 30-JAN-1998; 02-NOV-1998 06-AUG-1998. Mus sp.

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Glaser SM,
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                                                                                               This sequence reperesents the vitaxin antibody variable light chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically anglogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of anglogenesis, inflammatory diseases e.g. psoriasis, cancers and
integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 561; DB 19; 100.0%; Pred. No. 3.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitaxin light chain variable region protein.
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                                                                  Claim 1; Fig 1b; 129pp; English.
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Matches 107; Conser
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This sequence represents a LM609 grafted antibody variable light chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in
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fragments can be used in the diagnosis and treatment of abhavbeta.3-mediated diseases such as anglogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of such as diabetic retlinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
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                                                                                                                                                                                                                                                                                                                                                                          Length 107;
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                                                                                                                                                                                                                                                                                                                                                                          Score 561; DB 22;
Pred. No. 3.7e-36;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huse WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-437472/37
                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IXSY-) IXSYS INC.
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                                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                   osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-1997;
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the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                          1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their functional fragments. The antibodies or their functional fragments. The antibodies or their functional fragments. The diagnosis and treatment of alphaVbeta_3 mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to enhanced LM609 grafted antibodies
                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis.
                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                         1;
                                                                                                                                                                                    Score 555; DB 19;
Pred. No. 1e-35;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain variable region of LM609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB61364 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 7; 132pp; English.
                                                                                                                                                                                      98.9%;
99.1%;
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                                                                                                                                                                                                      Best_Local Similarity 99.1
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-050110/06.
                                                                                                                                       Sequence 107 AA;
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Sequence 107 AA;

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Gaps
                                                               EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence shows the humanised mature light chain variable region of the mouse CMV5 antibody. Murine CDRs were used in a human Wol framework to produce a pure humanised immunoglobulin (Ig) which is capable of binding to the 9H glycoprotein of cytomegalovirus. The Ig is non immunogenic, due to the human framework, and has a strong affinity for its predetermined antigen. They can be produced in large quantities via recombinant DNA and monoclonal antibody technology. The humanised Igs may be used alone or in combination with chemotherapeutic agents such as non-steroidal anti-inflammatory drugs or immunosuppressants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunoglobulin(s) having murine CDRs in human framework regions - have lower antigenicity; useful for treating e.g. HSV, CMV, T-cell disorders, myeloid disorders and auto-immune
                         ó
                                                                                                                                                                                                                                                                                            Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus; 9H; light chain; variable region; framework; human; Wol.
 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneider WP;
                          Indels
                                                                                                   RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                               Score 555; DB 22;
Pred. No. 1e-35;
0; Mismatches 1;
                                                                                                                                                                                                                                                                    Humanised VL region of the mouse CMV5 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Queen CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "mutated residue"
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                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                          AAR25729 standard; Protein; 107
98.9%;
larity 99.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                    "CDR"
                                                                                                                                                                                                                                                                                                                                                                                                              "CDR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      "CDR"
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/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-249842/30.
           al Similarity
106; Conserv
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  Query Match
              Local
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Matches
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6; Indels

Mismatches

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98; Conservative
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                           Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chalh; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
                                                                       Gaps
                                                                                                  1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                   Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell-
                                                                       ó;
                                           Length 107;
                                                                       Indels
                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                Humanised CMV5 antibody light chain SEQ ID NO: 63.
                                                                      ;
9
                                           DB 13;
                                        Score 512; DB 1
Pred. No. 2e-32;
                                                                      3; Mismatches
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                                                                                                                                                                                                                                                            AAB69678 standard; Protein; 107
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                                         91.3%;
91.6%;
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                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Queen CL, Selick HE;
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                                                       Local Similarity
nes 98; Conserv
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107
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28-SEP-1990;
19-DEC-1990;
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 Sequence
                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp.
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                                                                      Matches
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DB 22; Length 107;

512; DB 2; No. 2e-32;

Score Pred.

91.3%; 91.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; zheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CWV infection.
EIVLTOSPATLSLSPGERATLSCQASQSISNHLHWYQORPGQAPRLLIKYRSQSISGIPA 60
                                                        1 eivltgspgtlslspgeratlscrasgsisnnlhwygqkpggaprllikyasgsisgipd 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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91.6%; Pred. No. 2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Wol antibody light chain SEQ ID NO: 87.
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89US-0310252.
90US-0590274.
90US-0634278.
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28-SEP-1990;
19-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the light chain variable region (VL) of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody DIPIZHC 1-0. It is based on the VL sequence (VL) of human Rabba subgroup III kappa chain, with complementarity determining regions (CDRs) from the murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody DI2 (see AAW84093). 3 Murine framework recidus (1, 49 and 60) are retained. The humanised light chain can be expressed in host cells using nucleic acid molecules (see AAW4090) of the invention. Humanised DI2 VH is also provided (see AAW44097)). The humanised antibodies can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or angiogenic-related disorders, such as anglogenesis associated with diabetic retinopathy, atherosclerosis and restenosis, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone recorders and responsesis,
                                                                                                                                                                      Humanised antibody; monoclonal antibody; MAb; antibody engineering; mouse; human; vitronectin; alpha~v beta-3; receptor; restenosis; cancer: metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; bl2H2HC-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
            anti alpha_v beta_3 vitronectin receptor antibodies
                                                                                                                                            Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VL.
                                                                                                                                                                                                                                                                                                     Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 61-62; 97pp; English.
                                                                              AAW84098 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                      50..56
/label= CDR2
89..97
/label= CDR3
                                                                                                                                                                                                                                                                                                                24..34
/label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0039609
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jonak ZL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-034590/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV71800.
                                                                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                           15-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                             WO9840488-A1
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                                                                                                   AAW84098;
                                                                                                                                                                                                                                                                                                     Key
Region
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Gaps
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                          osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                        Humanised antibody, monoclonal antibody; MAb; antibody engineering;
mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
cancer; metastasis; rheumatoid arthritis; atherosclerosis;
hyperparathyroidism, Paget's disease, hypercalcemia of malignancy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New anti alpha_v beta_3 vitronectin receptor antibodies - used for
immunotherapeutic treatment of e.g. diabetic retinopathy,
inflammatory disorders, atherosclerosis, restenosis, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the region of the murine monoclonal antibody (MAb) D12 light chain variable region (VL) that is altered in humanised D12 VL (see also AAW8409B). A synthetic gene (see AAV81902) encoding the protein was prepared from synthetic oligonucleotides and used to prepare an expression vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3 vitronectin receptor MAb. Humanised D12 MAbs can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated
                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA
                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                               . 6
                                                                                                                                                                                                                       Score 510; DB 20;
Pred. No. 2.8e-32;
4; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitronectin alpha-v beta-3 MAb VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW84100 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                       90.9%;
ilarity 90.7%;
Conservative
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Best Local Similarity
Matches 97; Conserv
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                                                                                                                                       107
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The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor.
                                                                                                                                                                                                                                                                         Kappa; light chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementalty determining region; CDR.
21 eivltqspatlslspgeratlscrasqsigtnihwyqqrpgqaprllikyasesisgipa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric and humanised versions of anti-EGF receptor antibody 225 used for inhibiting tumour growth, esp. of late stage prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RKA. The MAb is specific for the human epidermal growth factor (EGF)
                                            Kappa light chain variable region of 225RA antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                 1..23
/label- framework_1
`24..34
/label- CDR_1
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                                                                                                                                                     AAW08948 standard; Protein; 107
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/label= 1
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/label= (
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/label- 1
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98..107
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07-JUN-1995;
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                                                                                                                       Gaps
                                                                                                       1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle
                                                                                                                                                                                                                                                                                                                                                                                             Kappa; light chain; reshaped; monoclonal; antibody; 225RA;
human; epidermal growth factor; EGF; receptor; inhibition; growth;
tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric and humanised versions of anti-EGF receptor antibody 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the reshaped human monoclonal antibody (MAb) H225, 225KKA. The MAb is specific for the human epidermal growth factor (EGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for inhibiting tumour growth, esp. of late stage prostatic
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                                              Length 112;
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                                                                          Indels
                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                   Kappa 11ght chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha JW;
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Pred. No. 5.5e-32;
6; Mismatches 5;
                                            Score 510; DB 20;
Pred. No. 2.9e-32;
                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones ST,
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                                            90.9%;
90.7%;
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95US-0482982.
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                                                                            Conservative
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Best Local Similarity 89.7
Matches 96; Conservative
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N-PSDB; AAT49345.
                                            Query Match
Best Local Similarity
Matches 97; Conserv
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 112
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07-JUN-1995;
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Length 107;

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Query Match

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AAW08949

RESULT

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Humanized antibody binding to verotoxin II used for treating Verotoxin producing E. \operatorname{coli} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1; monoclonal antibody; light chain; mouse; humanised antibody; human; Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
                           The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle
                                                                                                                                                                                                                                   1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse anti-verotoxin II antibody VTm1-1 humanised VL region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region
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 MAb is specific for the human epidermal growth factor (EGF)
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                                                                                                                                                                                                                                                                            RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                           Score 494; DB 18;
Pred. No. 4.6e-31;
6; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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(PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                         Query Match 88.1%;
Best Local Similarity 87.9%;
Matches 94; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US11179
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70..76
/note= "c
109..117
/note= "c
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                                                                                                                107 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                     inhibitor
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          AAY32407
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                                                                      Gaps
                                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                            Kappa; light chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric and humanised versions of anti-EGF receptor antibody 225 used for inhibiting tumour growth, esp. of late stage prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RKA. The
                                                                     ;
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                                        Score 501; DB 18; Length 107; Pred. No. 1.3e-31;
                                                                     Indels
                                                                                                                                                         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                       Kappa light chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saldanha JW;
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                              89.3%; Scor.
88.8%; Pred. No. ...
... 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldstein NI, Jones ST,
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/label= CDR_3
98..107
/label= framework_4
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/label= framework_2
50..56
/label= CDR_2
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/label= framework_1
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/label= framework_3
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                                                                                                                                                                                                                                                           AAW08949 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMCL.) IMCLONE SYSTEMS INC. (MRCC.) MRC COLLABORATIVE CENT.
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95US-0482982
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                                                                     95; Conservative
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                                                       Similarity
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107
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Key Region

Region Region Region Region Region Region

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Claim 26; Page 33-34; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                            Sequence
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                     This sequence represents a humanised light chain variable region of murine monoclonal antibody VTM1-1 (MuVTM1-1), an antibody that specifically binds to the B subunit of verocroxin II (VT2). The invention relates to humanised antibodies against VT2 that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVTM1-1 comprising the complementarity determining regions of MuVTM1-1 and the heavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain frameworks, provided that at least 1 position selected from L49, H29, H30, H49 and H38 is occupied by the amino acid at the equivalent constitution of the MuVTM1-1 antibody heavy or light chain variable region framework. Such humanized antibodies have an affinity for VT2 that is 3-, 5 or 10-times that of MuVTM1-1. They are used for treating a patient suffering from, or at risk of, the toxic effects from VT2 (claimed), especially for treating verotoxin producing Escherichia coll (VTEC) infection, and haemolytic uraemic syndrome (HUS).
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain variable region; chimeric antibody; anti-CD40 antibody; chil220; humoral immune response; T cell dependent antigen; collagen induced arthritis; transplant induced rejection; T cell mediated disorder; autolimnue disease; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                            Length 127;
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                                                                                                                                                                                                                                                                                                                            Score 490; DB 21;
Pred. No. 1.1e-30;
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Claim 12; Fig 2b; 59pp; English.
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89.7%;
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Best Local Similarity 89.7
Matches 96; Conservative
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N-PSDB; AAZ10205.
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                                                                                                                                                                                                                                                                                127 AA;
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The present sequence represents the variable light chain of humanised antibody 13.17. The antibody is effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the variable light chain of humanised antibody F4. The antibody is effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Light chain variable region; chimeric antibody; anti-CD40 antibody; chi220; humoral immune response; T cell dependent antigen; collagen induced arthritis; transplant induced rejection; T cell mediated disorder; autoimmune disease; inflammatory disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh
Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;
                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The variable light chain of humanised antibody F4.
                                                                                                                                                                                                                                                                           Score 489; DB 20;
Pred. No. 1.1e-30;
5; Mismatches 7;
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88.8%;
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                 transplantation.
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N-PSDB; AAZ10203.
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Best Local Similarity
Matches 95; Conserv
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anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases, and transplantation.

Sequence 107 AA;

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Gaps

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Length 107;

1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60

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Search completed: October 11, 2001, 12:01:58 Job time: 968 sec

Query Match 87.0%; Score 488; DB 20; Length 10 Best Local Similarity 88.8%; Pred. No. 1.3e-30; Matches 95; Conservative 5; Mismatches 7; Indels

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APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUMPALLEN.
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CONTELLEN.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC 1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATPONEY/AGENT INPORMATION:
APPLICATION NUMBER: 30,223
FILING DATE: 28-DEC-1988
ATPONEY/AGENT INPORMATION:
TELEPRAY: (415) 326-2420
INFORMATION CAPING SEQ ID NO: 63:
SEGUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-487-200-47
US-08-484-537-47
US-08-783-853A-57
US-08-232-081B-42
                          US-08-474-040-83
US-08-487-200-83
US-08-436-453-4
US-08-436-463-4
US-08-107-633-4
US-08-107-639-1
US-08-107-788A-1
US-08-477-788A-1
US-08-477-531B-1
US-08-477-531B-1
US-08-477-531B-1
US-08-477-728-47
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5-08-477-728-47
5-08-474-040-47
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MEDIUM TYPE: Floppy disk
CMBUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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      COUNTRY: U
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US-07-634-278-63
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Sequence 87,
Sequence 10,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                                GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
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US-07-634-278-87
US-08-477-728-87
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US-08-472-00-87
US-08-487-200-87
US-08-485-200-87
US-08-485-27-87
US-08-485-57-87
US-08-127-7218-10
US-08-127-7218-6
US-08-127-7218-6
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US-08-127-7218-8
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US-08-487-200-62
US-08-484-537-62
US-07-634-278-83
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                                                                                                                                                                                                                October 11, 2001, 12:01:06
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Database :

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111 112 113 114 116 117 118 119 119 119 125 127 127

Searched:

Sequence:

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Query Match 91.3%;
Best Local Similarity 91.6%;
Matches 98; Conservative
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US-08-477-728-63
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                                                                                                                                                                                                                                                                Score 512; DB 1; Length 107;
Pred. No. 5.6e-42;
3; Mismatches 6; Indels
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APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DE-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION NUMBER: US/O7/590,274
PRIOR APPLICATION NUMBER: US/O7/590,274
PRIOR APPLICATION NUMBER: US/O7/310,252
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US/O7/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US/O7/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM M
REGISTRATION NUMBER: 11823-002600
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPAX: (415) 326-2400
TELEFAX: (415) 326-2400
TELEFAX: (15 MARCHERISTICS:
TENETHER OF THE MATTOR INFORMATION:
TELEPAX: (115) 326-2400
TELEFAX: (115) 326-2400
TELEFAX: US/OF TELEPAX: US/O
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                                                                                                                                                                                                                                                                Query Match 91.3%;
Best Local Similarity 91.6%;
Matches 98; Conservative
                                                   ; MOLECULE TYPE: peptide US-07-634-278-63
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CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
linear
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TOPOLOGY: 1in
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US-07-634-278-87
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TOPOLOGY:
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                                                   Gaps
                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
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Score 512; DB 1; Length 107;
Pred. No. 5.6e-42;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK 107
                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                      Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: OUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
TITLE OF INFORTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11823-002600
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CLASSPETCATION: 424
PROR APPLICATION DATA:
APPLICATION NUMBER: 05 07/634,278
FILING DATE: 19-DEC-1990.
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 05 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGGRT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amin
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1. TELECOMMUNICATION INFORMATION
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Best Local Similarity 91.6%;
Matches 98; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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: California
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
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Patent No. 5693761

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: COLINGH, Kathleen L.

APPLICANT: OLINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: Palo Alto

CITY: Palo Alto

STATE: California
       61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK. 107
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ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLLASSIFICATION: 536
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
AUTONIEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 512; DB 1; L. 91.6%; Pred. No. 5.6e-42; Live 3; Mismatches 6;
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REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
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Best Local Similarity 91.6
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-474-040-63
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                                                                                  RESULT 5
US-08-474-040-63
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1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                             RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: SCHNEIDER, William P.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, William M
REGISTRATION UNBER: 30,23
REFERENCE/DOCKET UNBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-00N-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION UNDRER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION UNDRER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION DATA:

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FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             Sequence 87, Application US/08477728 Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid
TYPE: amino acid
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Matches 98; Conserv
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US-08-477-728-87
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COUNTRY:

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Gaps

Indels

61

Query Match

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Length 107;

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                                                                APPLICANT: OUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFWHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
91.3%; Score 512; DB 1;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PULICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 87, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION: APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63, Application US/08487200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID 0.: 87:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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STRANDEDNESS: si
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US-08-487-200-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 512; DB 1; Length 107;
Pred. No. 5.6e-42;
3; Mismatches 6; Indels
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APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: CADINGH Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SECUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPAILLLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING APPLICATION TATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTOMORY AGENT INFORMATION:
APPLICATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
RELEPONDE: (415) 326-2400
TELEFONDE: (415) 326-2402
INFORMATION FOR SEO ID NO: 63:
                                                                                                                                                                                      Townsend and Townsend and Crew
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                                                                                                                                                                                                                                                                                                   ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                              379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.3%;
91.6%;
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Best Local Similarity 91.65
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-487-200-63
                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-487-200-87
                                                                                                                                                                                                                                                                           COUNTRY:
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APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIETCATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 30-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 30-DEC-1988
APPLICATION NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

AUTHER: IBM PC COMPATIBLE

TOWN PC-DOS/MS-D
                                                                                                                                                                                                                                                 379 Lytton Avenue
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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TOPOLOGY: lir
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-484-537-63
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Pred. No. 5.6e-42;
3; Mismatches 6; Indels
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                       APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Wilcholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-002610
FELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/634,278 FILING DATE: 19-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/487,200 FILING DATE: 7-4101-1995 CLASSIFCATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 63, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.6%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                      379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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QUEEN, Cary L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                  Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                94301
                                                                                                                                                                                                                                                                                                                                                                             STATE: Co
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APPLICANT:
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Length 107;
                                               6; Indels
                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPHTFGQGTKVEIK 107
                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
Query Match
91.3%; Score 512; DB 4;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
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IBM PC compatible
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                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 127 amino acids TYPE: amino acid
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Best Local Similarity 86.0
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                   COMPUTER READABLE FORM:
                       East Hanover
                                                                                                                                       COMPUTER: IBM PC COPERATING SYSTEM:
                                             New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
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07936-1080
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ZIP: 07936-1080
                                                                                                                         MEDIUM TYPE:
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                                                             COUNTRY:
                       CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: KOLDINGET, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an IITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
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APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
HUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                             E: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                 SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,537
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Pred. No. 5.6e-42;
3; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
FILING DATE: 1000 NUMBER: 11823-002600
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ITELERAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.3%;
Best Local Similarity 91.6%;
Matches 98; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-484-537-87
                                                                                                                   CITY: Palo Alto
STATE: California
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                                                                                                                                                                           94301
                                                                           ADDRESSEE:
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US-08-476-176B-10
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                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08127721A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Raldman, No. 6066718man
APPLICANT: Raldman, No. 6066718man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 486; DB 2; Length 127;
Pred. No. 2e-39;
7; Mismatches 8; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,176B FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27 SEPTEMBER-1993
APPLICATION NUMBER: 108 07/952,802
FILING DATE: 25 SEPTEMBER-1992
ATORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4.19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPRAN: (908) 277-5110
TELEPRAN: (908) 277-4306
INFORMATION FOR SEQ. ID NO: 10:
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Gaps
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APPLICANT: Hardman, No. 5958708man
APPLICANT: Hardman, No. 5958708man
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                 Length 127;
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COMPUTER READABLE FORM:
MEDIUM TYED: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATREET: 59 Route 10
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
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PRIOR APPLICATION D478
PRIOR APPLICATION D478
PAPELICATION UMBER: 08/127,721
PILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTATION NUMBER: 33,200
REFERENCE/CDCCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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86.0%; Pred. No. 2e-39;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08476176B Patent No. 5958708
     INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.6%;
Best Local Similarity 84.1%;
Matches 90; Conservative
                                                      : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 127 amino acids
amino acid
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                               SEQUENCE CHARACTERISTICS
                                                                           TYPE: amino acid
TOPOLOGY: linear.
MOLECULE TYPE: protein
US-08-485-246A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-476-176B-6
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 92; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-476-176B-6
                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldan
APPLICANT: Saldan
APPLICANT: Saldan
TITLE OF INVENTION: Meshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 2e-39;
7; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PALENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DAIL. ... 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTONNEY/AGENT INFORMATION:
NAME: NO. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
; REFRENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECHONE: (908) 277-5110
; TELEFRAX: (908) 277-5110
; TELEFRAX: (908) 277-5110
; TELEFRAX: (908) 277-5110
; TELEFRAX: (108) 277-5110
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGBNT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
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ZIP: 07936-1080
COMPUTER READABLE FORM:
COMPUTER TEAPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DG
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(908) 277-4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 86.03
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-127-721A-10
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| Sequence 6, Application US/08127721A
| Sequence 6, Application US/08127721A
| Sequence 6, Application US/08127721A
| Sequence 6, Application US/08127721A
| Patent No. 6066718
| APPLICANT: Hardman, No. 6066718man
| APPLICANT: Saldanha, Jose
| TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
| TITLE OF INVENTION: Immunoglobulin isotype
| TITLE OF INVENTION: Ammunoglobulin isotype
| TITLE OF INV
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 480; DB 3;
Pred. No. 7.4e-39;
9; Mismatches 8
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REGISTRATION NUMBER: 33,200
REFERENCE/FOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.6%;
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Matches 90; Conservative
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MOLECULE TYPE: protein

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Search completed: October 11, 2001, 12:01:06 Job time: 916 sec gb_sts1:*
gb_sts2:*
gb_sts3:*

jb_sy:* jb_un:* jb_vi1:*

Sequence:

Run on:

Searched:

b_htg1:

em_pl:* em_ro:*

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em_sy:* em_un:* em_vi:

em_pat:*

us-08-791-391a-5.rge

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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                                                                                                            (without alignments)
2557.737 Million cell updates/sec
                                                                                          October 11, 2001, 15:09:31; Search time 2122.65 Seconds
                                                                                                                                                     US-08-791-391A-5
351
1 GAAGTGCAGCTGGTGGAGTC.......CTCTGGTCACTGTCTCTGCA 351
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                 1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Database :

3b_pr1

gb_htg11:*
gb_htg12:*
gb_htg13:*
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108289 Sequence 6 S45356 immunoglobu AX060780 Sequence A38870 Sequence 24 AR013776 Sequence M83724 Mouse monoc

A38870 AR013776 MUSIGMUD2A AR027762

108289 S45356 AX060780 AX060784 10

10 95

AX060784 Sequence

Description

SUMMARIES

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1.0	Query Match 100.0%; Score 351; DB 9; Length 351; Best Local Similarity 100.0%; Pred. No. 1.9e-109; Indels 0; Gaps Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0y 1 GAAGTGCGGGGGGGGTGTGAGGCTAAGGCTGGAAGCTCCTGAGATC 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	REFERENCE JULEASSILLEU. AUTHORS Zerler, B.D. TITLE An expression system for production of chimeric monoclonal antibodies JOURNAL Patent: EP 0380068-A1 6 01-AUG-1990; FEATURES Location/Qualiflers Source /Organism="unknown" BASE COUNT 112 a 116 c 130 g 124 t	Query Match 88.1%; Score 309.4; DB 10; Length 482; Best Local Similarity 92.6%; Pred. No. 4e-95; Aatches 325; Conservative 0; Mismatches 26; Indels 0; Gaps Qy 1 GAAGTGCAGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTGAAACTC 60	Qy 61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
883.6 883.6 882.6	ARO88763 Sequence ARO27763 Sequence ARI3106 Mus muscu AF113106 Mus muscu AF113106 Mus muscu AF113108 Mus muscu AE113108 Mus musculu S55737 VH-immunog1 UG2048 Mus musculu S79401 VH718-DSP2 M34737 Mouse Ig H- AF045519 Mus musculu ARO22566 Sequence S67234 IgG3-mucin E23342 Antibody ag E27111 Remedy for AF04552 Mus muscu AG2623 Sequence 42 X51721 Mouse mRNA X51721 Mouse mRNA X51721 Mouse mRNA X51721 Mouse mRNA X51724 Mus musculu AF04552 Mus muscul G2623 Sequence 38 M23677 Mus musculu AF04552 Mus musculu BF07592 DNA encodin S5676 anti-Lewis Z22142 M. Gomesticu AJ250759 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul AF0551 Mus muscul	N	ie; Murinae; Mu nucleic acids	t." KSLRLSCAASGFAFSSYDMSWVRQIPEKR NAKNTLYLQMSSLNSEDTAMYYCARHNYG
9 293.6 11 293.6 11 293.6 11 293.6 11 293.6 11 293.6 11 293.6 12 290.1 13 290.1 14 280.2 20 284.2 20 284.2 22 280.8 28 282.6 28 28 282.6 28 28 282.6 28 28 28 28 28 28 28 28 28 28 28 28 28 2	83.6 721 9 ARO 83.6 733 9 ARO 82.6 354 94 AF 82.6 354 94 AF 82.5 354 94 AF 82.5 598 95.5 598	AX060784 351 bp DNA Sequence 5 from Patent WO00786 AX060784.1 GI:12406164 house mouse. Mus musculus Bukaryota, Metazoa; Chordata;	Mammalla: Eutheria; Rodentia; 1 (bases I to 351) HUSE,W.D. and Wu.H. Antig(a) v7g(b)3? recombine encoding same and methods of Patent: WO 0078815-A 5 28-DEC. Applied Molecular Evolution (Location/Qualifiers	

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AX060780.1 GI:12406160
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synthetic construct
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TITLE
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SOURCE
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GRFSSIDMSWVRQPPEKRLEWVAYISSGGDNTYYPDTVKGRFTISRDNAKNTLYLQM
SSLKSEDTAVYCARRYGLPFAYWGGTLVTVSA"
116 c 113 g 126 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="immunoglobulin heavy chain variable"
/note="anti-human IL-2R; This sequence comes from Fig. 1b"
/codon_start=1
                                                                                                                                                                                                                                                                                                                           Shedd, D., Cahili, K. and Zerler, B.
Differential effects of a murine and chimeric mouse/human
anti-interleukin-2 receptor antibody on human T-cell proliferation
Immunology 76 (3), 452-459 (1992)
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 488)
                                                                                                                                          845356 488 bp mRNA ROD 08-MAY-1993 immunoglobulin heavy chain variable=anti-human IL-2R [mice, mRNA Partial, 488 nt].
                                                                                                                                                                                                                                                                                                                                                                                                GenBank staff at the National Library of Medicine created this entry [NCBI glubbsq 115041] from the original journal article. This sequence comes from Fig. 1b.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
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                Rose, B., Gillespie, A., Wunderlich, D., Kelley, K., Dzuiba, J.,
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/protein_id="AAB23305.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 309.4; DB 95; Length 488;
Pred. No. 4e-95;
0; Mismatches 26; Indels 0;
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80. .487
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/organism="Mus sp."
/db_xref="taxon:10095"
80. .487
/partial
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92.6%;
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/partial
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KEYWORDS
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/protein_id="cac24888.1"
/db_xref="cd::12406161"
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LEWVAKVSSGGGSTYYLDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYG
                                                                                                                                                                                                                                                                                                                                                                                                                                        Huse, W.D. and Wu, H.

Anti-g(a) v?_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
241 CTGCAAATGAGCAGTCTGAAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAACT 301
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                                                                                                                                                                                                                                             22-JAN-2001
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                                                                                  301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 351
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/note="grafted antibody variable region"
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/db_xref="taxon:32630"
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/gene="IgM"
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Hamann, P. Ross, Hinman, L., Hollander, I., Holcomb, R., Hallett, W.,
Tsou, H. and Weiss, M.J.
Conjugates of methyltrithio antitumor agents and intermediates for
their synthesis
Patent: US 5773001-A 56 30-JUN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GAAGTGAAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCTGAAACTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                Municipalitied.

Unclassified.

I (bases 1 to 413)

I (bases 1 to 413)

I (bases 1 to 413)

HUMANISED AWTIBODIES DIRECTED AGAINST A33 ANTIGEN PATENT: WO 9413805-A 24 23-JUN-1994;

CELLTECH LTD (GB)

Other publication A0 5656894 940704

Other publication A75043347 951318.

Location/Qualifiers
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     PAT
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                                                                                                                                                                                                                                                                                                                                Score 296.6; DB 9;
Pred. No. 9.7e-91;
0; Mismatches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR013776 413 bp DNA
Sequence 56 from patent US 5773001.
AR013776 GI:3971230
                                                                                                                                                                                                                                                /organism="unidentified"
/db_xref="taxon:32644"
99 c 118 g 106
                   WO9413805
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100 c 117 g
Sequence 24 from Patent A38870
                                                                                                                                                                                                                                                                                                                              84.5%;
90.3%;
                                           A38870.1 GI:2295288
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Unclassified.
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LEWVAEISSGGSYTYPDTVTGRFTISRDNAKNTLYLEMSSLRSEDTAMYYCARDGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide sequences from the hypervariable regions of two monoclonal anti-idiotypic antibodies against the thyrotropin (TSH) receptor are similar to TSH and inhibit TSH-increased cAMP production in FRTL-5 thyroid cells
J. Biol. Chem. 267 (9), 5977-5984 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 354)
Taub,R., Hsu,J.C., Garsky,V.M., Hill,B.L., Erlanger,B.F. and Kohn,L.D.
                                                                                                                                                                                                63 GAAGTGAAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCTGAAACTC 122
                                                                                                                                                                                                                                                                                                    121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
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D-region; Ig heavy chain; J-region; V-region; immunoglobulin;
immunoglobulin mu-chain; monoclonal antiidiotypic antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSIGMUDZA 354 bp mRNA ROD 08-MAY-200
MOUSE monoclonal antiidiotypic antibody IgM VDJ-region mRNA
M83724
                                                                                                                                                                                                                                                                                                                              TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
                                                                                                    1 GAAGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC
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  Length 413;
                                                    35; Indels
Score 295; DB 9;
Pred. No. 3.5e-90;
                                                  0; Mismatches
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/organism="Mus musculus"
/db_xref="taxon:10090"
/map="chromosome 6"
/cell_line="4G11"
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/protein_id="AAA53040.1"
/db_xref="GI:197952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hybridoma"
<1. .>354
/gene="IgM"
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84.0%;
90.0%;
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/gene="IgM"
                                                  Matches 316; Conservative
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                                                                                                                                               Score 294.8; DB 94; Length 354;
Pred. No. 4e-90;
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Pred. No. 1.1e-89;
); Mismatches 34
                                                                                                                                               84.0%; Scc. 91.5%; Pred. No. *C. 0; Mismatches
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WhitLow,M.D. and Filpula,D.R.
Thiker for linked fusion polypeptides
Patent: US 5856456-A 15 05-JAN-1999;
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310. .>354
/gene="IgM"
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Matches 324; Conservative
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TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
                                                                 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC
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Pred. No. 1.1e-89;
0; Mismatches 34;
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Whitlow,M.D. and Filpula,D.R.
Linker and linked fusion polypeptides
Patent: US 5990275-A 15 23-NOV-1999;
Location/Qualifiers
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AR088763
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Best Local Similarity 90.2%;
Matches 314; Conservative 0
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/protein_id="AD29596.1"
/db_xref="G1:4768653"
/db_xref="G1:4768653"
/tb_xref="G1:4768653"
/tb_ranslation="EVMLVESGGGLVKPGGSIKLSCAASGFTFSSYTMSWVROTPEKR
/twwnxprsscgggryyyyPDSVKGRFTISRDNAKNNLYLOMSSLRSEDTALYYCARGYYS
NYFAYWGGGTLVTVSA"
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/product="anti-myeloperoxidase immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                      AF113106 354 bp mRNA ROD 21-SEP-2000
Mus musculus hybridoma Y6-4B5 anti-myeloperoxidase immunoglobulin
heavy chain variable region mRNA, partial cds.
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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2 (bases 1 to 354)
3 Ucthwa, H.S., Nachman, P.H., Jennette, J.C., Falk, R.J., Kinjoh, K., Tuttle, R. and Taylor, J.
Direct Supmission
Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
Location/Qualifiers
                                                                                                                                     241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
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Jethway H.S. (larke, S.H., Itoh-Lindstrom,Y., Falk,R.J., Jennette,J.C. and Nachman,P.H.
Restriction in Wkappa gene use and antigen selection in anti-myeloperoxidase response in mice
J. Immunol. 165 (7), 3890-3897 (2000)
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llarity 90.7%; Pred. No. 1.8e-88;
Conservative 0; Mismatches 30;
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/db_xref="taxon:10090"
/cell_line="hybridoma Y6-4B5"
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Matches 321;
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                                                                                                                                                                             Score 293.6; DB 9
Pred. No. 1.1e-89;
0; Mismatches 34
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           1 (bases 1 to 733)
Whitlow,M.D. and Filpula,D.R.
Linker for linked fusion polypeptides
Patent: US 5856456 A 17 05-JAN-1999;
Location/Qualifiers
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WhitLow,M.D. and Filpula, D.R.
Linker and linked fusion polypeptides
Patent: US 5990275-A 17 23-NOV-1999;
Location/Qualifiers
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Seguence 17 from patent
AR088764
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90.28;
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Matches 314; Conservative
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'protein_id="AAD29597.1"

/db_xref="G1:4768655"

/translation="BYMLVESGGGLVKPGGSIKLSCAASGFTFSSYTMSWVROTPEKR LEWVATISSGGGNTYYPDSVKGRFTISRDNAKNNLYLOMSSLRSEDTALLYCARGYYS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Jethwa, H.S., Clarke, S.H., Itoh-Lindstrom, Y., Falk, R.J.,
Jennette, J.C. and Nachman, P.H.
Restriction in Vkappa gene and antigen selection in
                                                                                                                                                                                                                                                                                                               AF113107 354 bp mRNA ROD 21-SEP-2000
Mus musculus hybridoma Y6-8G3 anti-myeloperoxidase immunoglobulin
heavy chain varlable region mRNA, partial cds.
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Direct Submission
                                                                                                           61 TCCTGTGCAGCCTCTGGATTCACTTTCAGTAGCTATACCATGTCTTGGGTTCGCCAGACT 120
                               CCGGAGAAGAGGCTGGAGTGGGTCGCAAAGTTAGTAGTGGTGGTGGTGGTGCTACTAT 180
                                                             121 CCGGAGAAGAGCTGGAGTGGGTCGCAACCATTAGTAGTGGTGGTGGTAACACCTACTAT 180
                                                                                                                                                         241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
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1. 354 /organism="Mus musculus"
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Pred. No. 1.8e-88;
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/db_xref="taxon:10090"
/cell_line="hybridoma Y6-8G3"
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/note="VH 7183; anti-MPO"
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Best Local Simi
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/codon_start=1
/product=*anti=myeloperoxidase immunoglobulin heavy chain
/product=*cegion"
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LEWVATISSGGGNTYYPDSSVKGRFTISRDNAKNNLYLOMSSLRSEDFALYYCARGYYS
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Jethwa, H.S., Clarke, S. H., Itoh-Lindstrom, Y., Falk, R.J., Jennette, J.C. and Nachman, P.H.
Jennette, J.C. and Nachman, P.H.
anti-myeloperoxidase response in mice
J. Immunol. 165 (7), 3890-3897 (2000)
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Mus musculus hybridoma Y6-9G3 anti-myeloperoxidase immunoglobulin
heavy chain variable region mRNA, partial cds.
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Jethwa, H.S., Nachman, P.H., Jennette, J.C., Falk, R.J., Kinjoh, K.,
Tuttle, R. and Taylor, J.
Direct Submission
121 CCGGAGAAGAGGCCTGGAGTGGCTCGCAACCATTAGTAGTGGTGGTGGTAACACCTACTAT 180
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                                                181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
                                                                            181 CCAGACAGTGTGAAGGGTGGATTCACCATCTCCAGAGACAATGCCAAGAACAACGGTAC
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Pred. No. 1.8e-88;
0; Mismatches 30;
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/organism="Mus musculus"
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LEWVATISSGGSYTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCA"
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Komori, T., Sugiyama, H., and Kishimoto, S.
A novel, V.H.DJ; H to J-H joining that induces H chain production in an Ig-null immature B cell line an Ig-null immature B cell line 89309739
On Sep 24, 1994 this sequence version replaced gl:341843.
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Desement; J-segment; V-region; V-segment; immunoglobulin; immunoglobulin heavy chain.
Mus musculus (strain BALB/c, sub_species domesticus) newborn cDNA to mRNA.
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Mus musculus IgH chain A allele of AT8-1-12 mRNA,
M28187

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    /organism="Mus musculus"
    /strain="BALB/c"

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em_gss_fun:*
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em_gss_hum3:*

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em_gss_hum6; *
em_gss_hum6; *
em_gss_hum8; *
em_gss_hum9; *
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em_gss_lnv2; *
em_gss_lnv2; *
em_gss_pln1; *
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252: em_gss_inv4;*
253: em_gss_inv4;*
254: em_gss_rod6;*
255: em_gss_rod7;*
256: gb_gss35;*
257: gb_gss35;*
258: gb_gss37;*

gb_gss32: gb_gss33: gb_gss34:

9b_9ss8:*
9b_9ss9:*
9b_9ss10:*
9b_9ss11:*
9b_9ss12:*
9b_9ss13:*
9b_9ss16:*
9b_9ss16:*
9b_9ss16:*
9b_9ss21:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score

Result õ 266.4 260.8 258.6 258.6 258.6 258.6 255.8 255.8

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/strain="C2ECH II"
/db_ref="taxon:10090"
/clone="IHAGE:4020753"
/clone=lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/tasue_type="tumor, metastatic to provide in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the image in the imag
Email: cgapbs-r@mail.nih.gov

Tissue Producement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

found through the I.M.A.G.B. Consortium/LLNL at:

http://imaqe.llnl.gov a column: 10

Plate: LLAM9275 row: a column: 10

High quality sequence stop: 644.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1559)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGAGAAGAGGCTGGAGTGGCTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.0%; Score 277.4; DB 145; Length 877; Best Local Similarity 90.4%; Pred. No. 4.4e-75; Matches 319; Conservative 0; Mismatches 31; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 ACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTGCA 351
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

DEFINITION ACCESSION VERSION

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                    Concact: Noner: Strangery, Pn.D.

Consortium (11)

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONE dibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Troyte Genomics, Inc.

Clone distribution: NOT-CGAP clone distribution information can be http://image.lln.gov

Plate: Libraryed row: J column: 24

High quality sequence stop: 562.

Location/Qualifiers

J. 1559

Location/Qualifiers

J. 1559

Location/Qualifiers

J. Clone-lib-"NOT-CERF II"

/ Strain="Czech II"

/ Strain="Czech II"

/ Alab-Not-"Bullog"

/ Clone-lib-"NOT-CGAP-Lu30"

/ Clone-lib-"NOT-CGAP-Lu30"

/ Clone-lib-"NOT-CGAP-Lu30"

/ Lissue_type-"tumor, metastatic to mammary"

/ Jab_host-"Pullog"

/ Clone-lib-"NOT-CGAP-Lu30"

/ Lissue_type-"tumor, metastatic to mammary"

/ Jab_host-"Pullog"

/ Clone-lib-"NOT-CGAP-Lu30"

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 494)
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        Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                      Other_ESTS: uu72g05.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                    Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Image.llnl.gov/Image/html/iresources.shtml
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            1 (bases 1 to 404)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                            /strain="CZECH II (feral)"
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/clone="IMAGE:3675897"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo Clibrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

94 c 109 g 105 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 2.4e-69;
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/organism="Mus musculus"
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Seq primer: -40RP from Gibco
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91.98;
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/organism="miscurus"
//organism="miscurus
//db_xref="taxon:10090"
//clone="lubae:618594"
//clone="lubae:618594"
//clone="lubae:files"
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//dev_stage="type="spleen"
//dev_stage="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="ty
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Mus musculus

Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(Dases 1 to 469)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashUrNCI Mouse EST Project 1999

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine,
4444 Forest Park Parkway, Box 8501, St. Louis, MO
T=1: 314 286 1800
Fax: 314 286 1810
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91.9%; Pred. No. 2.5e-69;
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Location/Qualifiers
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Matches 273; Conservative
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CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
                       Query Match 72.9%;
Best Local Similarity 83.6%;
Matches 290; Conservative
                                                                                                                                                                                                                                                                            mRNA sequence.
BF582912
                                                                                                                                                                                                                                                                                                                                               house mouse.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                               AA170256 823 bp mRNA EST 16-FEB-1997 mm87910.11 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:618594 5. similar to gb:x14584 IG HEAVY CHAIN PRECURSOR V-III REGION (HUMAN); gb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the C-terminus (MOUSE);, mRNA sequence.
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GACGTGAAGCTGGTGGAGTCTGGGGAAGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTC 177
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                                                                                                                                                                                                                                                                                                                    The WashD-HMI Mouse EST Project Unpublished (1996)
Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 823;
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Pred. No. 2.9e-69;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector to vector length is 867
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.
Location/Qualifiers
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                                                                                                                              AA170256.1 GI:1748794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.7%;
Best Local Similarity 91.9%;
Matches 273; Conservative
                                                                                                                                                            house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                          Waterston, R.
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ISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mumalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CE 1 (bases 1 to 886)

I (bases 1 to 886)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLAM9814 row: j column: 15

High quality sequence stop: 718.

SS

Location/Qualifiers

Jucce

Annowing Missue Missuellus*
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/clone="IMAGE:4224494"
/clone="IMAGE:4224494"
/clone="lb="NCI-GAD=CO24"
/lab_host="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="b
181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC 240
                                                             298 GCAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAGGAACACCCTGTAC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                                                                                                                                                             DB 150; Length 886;
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Pred. No. 2.2e-68;
0; Mismatches 57
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/strain="FVB/N"
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181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC 240
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AUTHORS
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JOURNAL
                                                                                          241
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/clone="INAGE:002459"
/clone_lib="NCI_CGAP_LU30"
/tissue_type="tumor, metastatic to mammary"
/tissue_type="tumor, metastatic to property tissue_type="tumor, metastatic to mammary"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
3 a 271 c 267 g 201 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imagelln.gov

Plate: LLAM9279 row: h column: 12

High quality sequence stop: 711.
                                                                                                                                                                                                                                                                                BF142302 1012 bp mRNA EST 24-OCT-2000 601791844F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4022459 5', mRNA sequence.
BF142302
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1012)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                        241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                                                                                                   358 TACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTC 404
                                                                                                                                               301 TACGGCAGTTTTGCTTACTGGGGCCCAAGGGACTCTGGTCACTGTCTC 347
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Pred. No. 4e-68;
0; Mismatches 60;
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1. .1012
/organism="Mus musculus"
/strain="CZECH II"
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ilarity 82.9%;
Conservative
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/lab_host="DH10B (Tl_phage-resistant)"
/note="Organ: colon; Vector: pCWV-SPORTS; Site_1: NotI;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

a 200 c 201 g 182 t
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1 (bases 1 to 774)

1 (bases 1 to 774)

Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                               CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
                                                                                                             þe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jéffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can hfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9813 row: j column: 14
High quality sequence stop: 675.
1 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 150; Length 774;
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                                                                                                                                                                                      401 TACTCCCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA
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90.9%; Pred. No. 4.3e-68;
Live 0; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:4224109"
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1...774
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BF581450
BF581450.1 GI:11655162
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241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGAC---- 295
                                       ----ATAACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
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Best Local (
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KEYWORDS
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TITLE
JOURNAL
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                                                                                                                                                                                                           BF579001
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S NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9204 row: 1 column: 21
High quality sequence stop: 658.
                                                                                                                                                                                                         BF163874 662 bp mRNA EST 30-OCT-2000 601772386F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991460 5', mRNA sequence.
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/clone="IMAGE:3991460"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
Jab host="bylos"
/note="organ: lung; Vector: pcMV-SPORT6; Site_1: Sall;
Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
1 166 c 183 g 157 t l others
181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC 240
                   300 CCAGACAGTGTGAGGGGTCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                             241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.4%; Score 254.2; DB 145; Length 662; 85.8%; Pred. No. 6.3e-68; 1ve 0; Mismatches 39; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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ORIGIN
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AUTHORS
TITLE
JOURNAL
                                                                                                             358
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BF579001 650 bp mRNA EST 12-DEC-2000 602096117F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4215844 5',
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/dD_xref="taxon:10090"
/clone="imAdS:14215844"
/clone=lib="NcI_CGAP_CO24"
/clone=lib="NcI_CGAP_CO24"
/clone=lib="NcI_CGAP_CO34"
/clone=lib="NcI_CGAP_CO34"
/lab_host="bHI0B (TI phage-resistant)"
/note="lorgan: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.6 Kb. Constructed by Life
Average insert size 1.6 Kb. Constructed by Life
- Technologies. Note: this is a NCI_CGAP Library."
- 177 c 165 g 154 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 650)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue producement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9792 row: b column: 05
High quality sequence stop: 649.
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49; Indels
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Pred. No. 2e-67
0; Mismatches
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/organism="Mus musculus"
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84.6%;
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297; Conservative
                                                                                                                                                                                                                                               mRNA sequence.
BF579001
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BF162056 913 bp mRNA EST 30-OCT-2000 601768714F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3987986 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.inh.gov.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9195 row: I column: 03
High quality sequence stop: 581.
Location/Qualifiers
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1 248 c 260 g 187 t
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NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tlssue_type="spontaneous tumor, metastatic to mammary.
Stem cell orlgin."
/lab_host-"DH10B."
  296 CTAGACATTATAAAGGGCCGATTCACCATCTCCAGAGACAATGTCAAGAACATCCTGTAT 355
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                                          416 GATGACGCCTGGTTTACTGGGGCCAAGGGACTCTGGTCTCTCGCA 469
                                                                                                                                298 AACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTGCA 351
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85.3%; Pred. No. 6.7e-67;
iive 0; Mismatches 40;
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/strain="C2ECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3987986"
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Best Local Similarity 85.3
Matches 308; Conservative
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                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BF162056
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AUTHORS
TITLE
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COMMENT
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                                                                                                                                                                                                                                       BF180238 904 bp mRNA EST 31-OCT-2000 001806516F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4037595 5'
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 90).
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGAGAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
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Pred. No. 2.5e-67;
0; Mismatches 46; Indels 4;
                                                                                                           423 CATCTGACTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 473
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                                                                                   301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
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http://image.llnl.gov
Plate: LLAM9314 row: o column: 04
High quality sequence stop: 723.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C5786"
/db_xref="taxon:10090"
/clone="IMAGE:4037595"
/clone_lib="NCT_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/lab_hsst="DH108"
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Best Local Similarity 85.9%;
Matches 304; Conservative
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AUTHORS
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LOCUS RESULT 14

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ORGANISM

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ACCESSION VERSION KEYWORDS SOURCE

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ESM MUS musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 862)

8 NIH-MGC http://mgc.nci.nih.gov/.

8 NIH-MGC http://mgc.nci.nih.gov/.

8 National Institutes of Health, Mammalian Gene Collection (MGC)

8 Oppublished (1999)

8 Contact: Robert Strausberg, Ph.D.

8 Email: cgapbs-remail.nih.gov

8 Tissue Procurement: Gilbert Smith, Ph.D.

8 Contact: Robert Strausberg, Ph.D.

8 Email: cgapbs-remail.nih.gov

8 Tissue Procurement: Gilbert Smith, Ph.D.

8 Contact: Robert Strausberg, Ph.D.

8 Email: cgapbs-remail.nih.gov

9 Tissue Procurement: Gilbert Smith, Ph.D.

9 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

9 Http://mage.llnl.gov

10 July 11 July 12 July 12 July 13 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 July 14 Ju
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/tissue_type="tumor, metastatic to mammary"
/tissue_type="tumor, metastatic to mammary"
/tab_nost="bullog"
/nab_nost="bullog"
/note="Organ: lung; Vector: pcNV-SPORT6; Site_1: Not1;
Site_2: Sall; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. Library constructed by Life Technologies.
drivestigator providing samples: Gilbert Smith, NIH"
236 c 236 g 176 t lothers
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601786493F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014430
241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGAC---AT 297
                                                                                                                                                               172 TCCTGTGCAGCCTCTGGATTCACTTTCAGTGACTATGGAATGCACTGGGTTCGTCAGGCT
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82.7%; Pred. No. 9.7e-65;
live 0; Mismatches 60;
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/db_xref="taxon:10090"
/clone="IMAGE:4014430"
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Matches 291; Conservative
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AWB24857 454 bp mRNA EST 17-MAY-2000 us08c01.yl Scares_NMGBC_B-cell Mus musculus cDNA clone IMAGE:3166464 5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence. AW824857
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
CAGACAGTGTAGAGGGTCGATTCACCATCTCCAGAGACAAGGCCAAGAACACCCTGTAC 363
                                                                                                                                   296 ----ATAACTACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTGC 350
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85.1%; Pred. No. 9.9e-67;
iive 0; Mismatches 48; In
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/organism="Mus musculus"
/ob_xref="taxon:10090"
/clone="IMAGE:3166464"
/clone_lib="Soares_NMGBC_B-cell"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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159 TCCTGTGCAGCCTCTGGATTCACTTTCAGTGACTATGGAATGCACTGGGTTCGTCAGGCT 218
                                                              121 CCGGAGAAGAGGCTGGAGTGGCTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "LM609 antibody heavy chain variable region"
/note= "partial sequence, no start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LM609 antibody heavy chain variable region DNA fragment.
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re greater than or equal to the score of the result being printed,
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1 GAAGTGCAGCTGGAGTC......CTCTGGTCACTGTCTGCA
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                              IM609 and the antibody vitaxin bind selectively to integrin alphabetas and can be used to inhibit binding of alphabeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphabeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of IM609 have affinity more than 90 times greater than that of parent the parent antibody.
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                                              Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                          1 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC 60
                                                                                                                                    sequence encodes the LM609 antibody variable heavy chain region
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                                                                                                                                                                                                                                                                                                                        100.0%; Score 351; DB 19;
100.0%; Pred. No. 4.7e-95;
ive 0; Mismatches 0;
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                                                                                                            Claim 37; Fig 2a; 129pp; English.
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                                                                                      anglogenesis or restenosis
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC
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100.0%; Pred. No. 4.7e-95;
ive 0; Mismatches 0;
                                                                                                        (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 132pp; English
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23-JUN-2000; 2000WO-US17454
                                                     99US-0339922
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Best Local Similarity 100.0%,
Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1990 (first entry)
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                                                                                                                                                                                                                 WPI; 2001-050110/06.
                                                     24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                     osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ0555;
                                                                                                                                                              Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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AND DESCRIPTION OF THE PARTY OF

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/*tag= a
/product= "vitaxin antibody heavy chain variable region"
/note= "partial sequence, no start or stop codon given"
                                 Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the vitaxin antibody variable heavy chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 aggigcagciggiggagicigggggggggggttgigcagcciggaaggicccigagactci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGGCTGGAAGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgggcaagggtctggagtgggtcgcaaaagttagtagtggtggtggtagcacctactatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
Vitaxin antibody heavy chain variable region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.5e-80;
0; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.1%; Score 302.2; 91.9%; Pred. No. 1.5
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig la; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    97US-0791391
                                                                                                                                                                                                                                                                                                                                                                98WO-US01826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 91.9
Matches 319; Conservative
                                                                                                                                                                                                  1..351
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glaser SM, Huse WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-437472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (IXSY-) IXSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW76001
                                                                                                                                                                                                                                                                                          WO9833919-A2
                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                30-JAN-1998;
                                                                                                                                                                                                                                                                                                                              06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                                                                   Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ccagacactgtgaagggccgattcaccatctccagagacaatgccaagaacaccctttac 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTGAGACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAbs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MAbs, which have a longer serum half-life. Method can be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 309.4; DB 1
Pred. No. 1.2e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                  Location/Qualifiers
75..482
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.1%;
92.6%;
                                                                                                                                                                                                                                                       89US-0301216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 351
                                                                                                                                                                                                                                    89US-0441702
                                                                                                                                                                                                90EP-0101351
                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR THERAPEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-232892/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV49820 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; ; p;
                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR06251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 325;
                                                                                                                                                                                                24-JAN-1990;
                                                                                                                                                                                                                                                     24-JAN-1989;
                                                                                                                                                                                                                                    04 - DEC - 1989;
                                                                                                                                                            01-AUG-1990
                                                                                                                      EP380068-A.
                                                                                                                                                                                                                                                                                                                          Zerler B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV49820;
                Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312
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ID AAV4
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AC AAV4
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Gaps

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Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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/*tag=
6..62
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adair JR, King DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-217881/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR56962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1992;
22-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9413805-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                  AAQ68650;
                                         182
                                                                                                                                                                                                                            RESULT
AAQ68650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -
242 TGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAACT 301
              CCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CGÇAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 aggtgcagctggtggagtctggggggggggttgtgcagcctggaaggtccctgagactct 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 351;
                                                                                                                                                                                                                                                                 LM609; grafted antibody; alphavbeta_3 integrin; anglogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                   302 ACGGCAGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 302.2; DB 2
Pred. No. 1.5e-80;
0; Mismatches 28
                                                                                                                                                                                                                                         Vitaxin heavy chain variable region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 132pp; English.
                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.1%;
Best Local Similarity 91.9%;
Matches 319; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-2000; 2000WO-US17454;
                                                                                                                                                     AAF28175 standard; DNA; 351
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0339922
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-050110/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu H;
                                                                                                                                                                                                                                                                                                                                       WO200078815-A1.
                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis
                                                                                                                                                                                                             03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000,
                                                                                                                                                                                 AAF28175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huse WD,
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Polymerase chain reaction; primer; amplify; PCR; variable region; light; heavy; chains; VL; VH; humanised; antibody; vectors; expression; human; secretion; A33; Fab/(gamma4deltacys); pGC16; ompA signal; C-kappa; pSKompA; pMRR055; CHI domains; hinge; deltacys; pMRR022; pRO109; antigen; diagnosis; treatment; colorectal cancer; metastases; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAQ68649-50 encode the light and heavy chain variable regions (VM and VL) of the humanised anti-A33 antibody of the invention. These fragments were produced by PCK using the primer sequences given in AAQ68644.48. The amplified fragments were used in the construction of vectors for the expression and secretion of the
                                                                                                                                                                             301
                              242 TGCAAATGAGCAGTCTGAACTCTGAGGACACGCCATGTATTACTGTGCAAGACATAACT
TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                                                                                                       302 ACGCCAGTTTTGCTTACTGGGGCCCAAGGGACTCTGGTCACTGTCTCT 348
                                                                                                                                                                                                                                                               MAb A33 heavy chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 3(ii); 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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93GB-0015249.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ68650 standard; DNA; 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-GB02529
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chimeric humanised A33. The amplified products were cleaved with BstBI and SplI for the light chain and HindIII and ApaI for the heavy chain. These fragments were cloned into the human kapa light chain acceptor vector, pMRRI5.1, and the human heavy chain, IgG1, acceptor vector, pMRR011 respectively, to give chimeric expression vector pR0108 for the light chain and pR0107 for the heavy chain. Proteins which bind the A33 antigen can be used in the diagnosis or treatment of colorectal cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362
                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                         TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                                                                                                                                                                                                                                                                                     CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for peptide linker 212"
                                                                                                                                                                      DB 15; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; multichain protein; immunoglobulin; single chain antibody Fv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/note= "sequence coding for A33 Vh region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note- "the start codon is not indicated"
                                                                                                                                                                                                Indels
                                                                                                                            Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;
                                                                                                                                                                    Score 296.6; DB 15;
Pred. No. 7.2e-79;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "A33/212 scFv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "sequence coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A33/212 single-chain Fv coding sequence
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1..711
/*tag= a
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                                                                                                                                                                   Query Match 84.5%;
Best Local Similarity 90.3%;
Matches 317; Conservative
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The invention is directed to a novel peptide linker useful for connecting polypeptide constituents into a novel linked fusion polypeptide. The peptide linker includes at least one XP motif (where X is a charged amino acid) and includes any of these sequences (GSYSGSARCSGSGEGSTKG; GTSGSXRSGSEGSTKG; or GSTSGKSEGKG) to inhibit its proteolysis by subtilisin or trypsin. DNA molecules encoding fusion polypeptides, containing two polypeptides, derived from the same multichain protein of the immunoglobulin (1g) superfamily and a peptide linker as above, are particularly useful for diagnosis and treatment of cancer. The fusion polypeptide containing the specified linkers is proteolytically stable sassociated with positioning of the P residue's minoraction, while residue X improves solubility. The present sequence represents the nucleotide sequence of a A33/212 scfv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 gaagtgaagettgtggagtetggggggaggettagtgaageetggagggteeetgaaaete 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 teetgtgeageetetggattegettteagtacetatgaeatgtettggggttegeeagaet 483
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                                                                                                                                                                                                                                                                                                  A encoding fusion polypeptide including protease resistant linker for making single-chain Fv antibody fragments, e.g for diagnosis d treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 ccggagaagaggctggagtgggtcgcaaccattagtagtggtggtagttacacctactat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 ctgcaaatgagcagtctgaggtctgaggacacggccttgtattactgtgcaccgactacg
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Pred. No. 6.6e-78;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCT 348
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                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 12; 39pp; English.
                                                                                        94US-0224591.
92US-0980529.
93US-0002845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 83.6%;
Best Local Similarity 90.2%;
Matches 314; Conservative
                                                       94US-0224591
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                                                                                                                                                                     (ENZO-) ENZON INC.
                                                                                                                                                                                                                                                              P-PSDB; AAW95440.
                                                     07-APR-1994;
                                                                                        07-APR-1994;
20-NOV-1992;
                                                                                                                                                                                                           DR,
                 05-JAN-1999
                                                                                                                                15-JAN-1993
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BP

AAZ37397 standard; DNA; 721

AAZ37397

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Key
            AAV99766
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                                                                                                                                                                                                                                                                                                                                                                                                       for connecting
                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes a linked fusion protein containing the amino acid linker of the invention. The linkers are used for connecting constituent polypeptides to form novel linked fusion polypeptides. Polypeptides derived from any protein can be connected, in particular multichain protein or protein complexes e.g. enzymes, members of the immunoglobulin superfamily, hormones, DNA-binding proteins. The linker provides fusion proteins which have greater stability and are less
                                                                Fusion protein; linker; linked fusion polypeptide; multichain protein; protein complex; antibody; ss.
                                                                                                                                                                                                                                                                                                                              Peptide linkers, linked fusion polypeptides containing the linkers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACATGCCAAGAACACCCTATAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 293.6; DB 21; Length 721;
Pred. No. 6.6e-78;
0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;
                                              Linked fusion protein A33/212 sFv coding sequence.
                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 12; 42pp; English.
                                                                                                                                                                                                      94US-0224591.
92US-0980529.
93US-0002845.
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90.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            susceptible to aggregation.
                        (first entry)
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Best Local Similarity 90.2
Matches 314; Conservative
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                                                                                                                                                                                                                                                                               Whitlow
                                                                                                                                                                                                                                                                                                      WPI; 2000-022812/02.
                                                                                                                                                                                                                                                                                                                                         their preparation -
                                                                                                                                                                                                                                                         (ENZO-) ENZON INC.
                                                                                                                                                                                10-SEP-1997;
                                                                                                                                                                                                       07-APR-1994;
20-NOV-1992;
                      08-FEB-2000
                                                                                                                                US5990275-A.
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                                                                                                           Synthetic.
AAZ37397;
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The invention is directed to a novel peptide linker useful for connecting polypeptide constituents into a novel linked fusion polypeptide. The peptide linker includes at least one XP motif (where X is a charged amino acid) and includes any of these sequences (GSTSGSARGSGSGEGTKG; GTSGSXRSGSGEGTKG; CTSGSXRSGSGEGTKG; CTSGSXRSGGGTKG; OT GTSGKSEGKG) to inhibit its proteolysis by subtilisin or trypsin. DNA molecules encoding fusion polypeptides containing two polypeptides, derived from the same multichain protein of the immunoglobulin (1g) superfamily and a peptide linker as above, are particularly useful for diagnosis and treatment of cancer. The fusion polypeptide containing the specified linkers is proteolytically stable associated with positioning of the presidue; and resistant to aggregation, while residue X improves solubility. The present sequence represents the nucleotide sequence of a A33/218 scFv fragment.
                                                                                                                                                                                                                                     Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFV; multichain protein; immunoglobulin; single chain antibody FV; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A encoding fusion polypeptide including protease resistant linker for making single-chain Fv antibody fragments, e.g for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "sequence coding for peptide linker 218"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "the start codon is not indicated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "sequence coding for A33 Vl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A33/218 scFv"
                                                                                                                                                                             A33/218 single-chain Fv coding sequence.
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BP
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92US-0980529.
93US-0002845.
AAV99766 standard; DNA; 733
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
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20-NOV-1992;
15-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                          AAV99766;
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DB 20; Length 733;

Score 293.6;

83.68;

Query Match

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Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;
                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                              AAV07642;
                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes a linked fusion protein containing the amino acid linker of the invention. The linkers are used for connecting constituent polypeptides to form novel linked fusion polypeptides. Polypeptides derived from any protein can be connected, in particular multichain protein or protein complexes e.g. enzymes, members of the immunoglobulin superfamily, hormones, DNA-binding proteins. The linker provides fusion proteins which have greater stability and are less susceptible to aggregation.
                                                                                                                                                                                                                                                                                                                                                                       protein; linker; linked fusion polypeptide; multichain protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide linkers, linked fusion polypeptides containing the linkers and
                                              376 gaagtgaagcttgtggagtctgggggggggcttagtgaagcctggagggtccctgaaactc 435
                                                                  TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                             CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTAT 180
                                                                                                                 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC 240
                                                                                                                                                                                  CTGCAAATGAGCAGTCTGAACTCTGAGGACACACCATGTATTACTGTGCAAGACATAAC 300
                                                                                                                                                                                            Gaps
                             GAAGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC 60
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                                                                                                                                                                                                                       301 TACGGCAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCT 348
                                                                                                                                                                                                                                  6.6e-78;
ches 34; Indels
                                                                                                                                                                                                                                                                                                                                                   Linked fusion protein A33/218 sFv coding sequence.
          Mismatches
Pred. No.
          ö
                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                  protein complex; antibody; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0224591.
92US-0980529.
93US-0002845.
 90.2%;
                                                                                                                                                                                                                                                                                           AAZ37398 standard; DNA; 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97us-0926789
                                                                                                                                                                                                                                                                                                                                 08-FEB-2000 (first entry)
          Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Filpula DR, Whitlow MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-022812/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   their preparation -
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ENZO-) ENZON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY54837
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20-NOV-1992;
15-JAN-1993;
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anti-CD22 monoclonal antibody heavy chain variable region DNA sequence.
                                                                                                                                                          376 gaagtgaagcttgtgggagtctgggggaggcttagtgaagcctggagggtccctgaaactc 435
                                                                                                                                                                                                                   TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                                                                                                                                                                                               CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 ctgcaaatgagcagtctgaggtctgaggacacggccttgtattactgtgcaccgactacg 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-CD22 monoclonal antibody heavy chain variable region; VL; Pseudomonas exotoxin; variable heavy chain; VH; variable light chain; malignant B-cell; immunodiagnosis; RFB4 IgG; ss.
                                                             Gaps
                                                                                                             9
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                                                                                                          1 GAAGTGCAGCTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                       ccggaqaagaggctggaqtggttcgcaaccattagtagtggtggtagttacacctactat
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        Length
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/note= "CDS does not contain a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  676 gtagtcccgtttgcttactggggccaagggactctggtcactgtctct 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TACGGCAGTTTTGCTTACTGGGGCCCAAGGGACTCTGGTCACTGTCTCT 348
                                                           34; Indels
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        21;
Score 293.6; DB 2
Pred. No. 6.6e-78;
); Mismatches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
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     83.6%;
90.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US05453.
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                                                        Matches 314; Conservative
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P-PSDB; AAW66099.
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Otten GR;

Greenburg GB,

Finer MH,

97US-0815030 98WO-US03797

14-MAR-1997;

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(CASE/) CASENTINI-BOROCZ

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(FINE/) FINER M H.
(GREE/) GREENBURG G B.
(OTTE/) OTTEN G R.
                                                                                                                         Casentini-Borocz D,
                                                                                                                                             WPI; 1998-521211/44.
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                              13-MAR-1998;
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                                    (RFB4 IgG) heavy chain variable region DNA sequence. The invention claims for a recombinant immunoconjugate comprising of a therapeutic agent (e.g. pseudomonas exotoxin) or a detectable label peptide bonded to a recombinant anti-CD22 antibody hing a variable heavy (VH; AAW66099) chain with a cysteine residue at amino acid 44 and a variable light (VL; AAW66098) chain with a cysteine residue at amino acid 100. The immunoconjugate is claimed to inhibit the growth of malignant B-cells in vivo, such as rodent, canine or primate B-cells. The anti-CD22 antibody is claimed useful for detecting CD22 protein in a sample or in vivo in a mammal, and can be used in diagnostic kits.
                                                                                                                                                                                                                                                                    TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric receptor; A33; colorectal cancer; antigen; tumour; cytolysis; gene therapy; signal transduction; monoclonal antibody;
                                                                                                                                                                                                                                       CCGGAGAAGAGGCTGGAGTCGCTAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT
                                                                                                                                                                                                                                                                                                                               121 ccggagaagaggctggagtgggtcgcatacattagtagtggtggtggtaccacctactat
                                                                                                                                                                                                                                                                                                                                                  181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCCAGAGACAATGCCAAGAACACCCTATAC
                                                                                                                                                                                                                                                                                                                                                              ccagacactgtgaagggccgattcaccatctccagagacaatgccaagaacaccctgtac
                                                                                                                                                                                                                                                                                                                                                                                           CTGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC
                              The present sequence represents the anti-CD22 monoclonal antibody
                                                                                                                                                                                                          18;
                                                                                                                                                                                    Sequence 369 BP; 83 A; 85 C; 110 G; 91 T; 0 other;
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7..1938
/*tag= a
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         Fig 1; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV58929 standard; DNA; 1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A33 chimeric receptor DNA.
                                                                                                                                                                                     Query Match 82.9
Best Local Similarity 89.7
Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Mus sp.
Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 gtctctgca 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-1999
         Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV58929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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This DNA sequence codes for murine A33 chimeric receptor (see AAW73048) comprising a signal peptide from the Vkappa chain of human antibody 98-6. light chain and heavy chain variable regions of antibody 98-6. light chain and heavy chain variable regions of antibody 98-6. light chain and heavy chain variable regions of antibody 93. human colon cancer antigen A33 murine monoclonal antibody A33, human cg2 constant domain and M1 segment, human CD4 transmembrane domain cg6 constant domain portion of human TCR-associated zeta chain. A humanised version of the A33 chimeric proteins, and DNA encoding them, are constructed manner, a transmembrane domain and a cytoplasmic domain capable of binding to A33 in a non-MHC restricted manner, a transmembrane domain and a cytoplasmic domain capable of activating a signalling pathway. Binding of A33 to the extracellular domain results in transduction of a signal and a cytoplasmic domain capable of activating a signalling pathway in the cell, such that the cell may be induced to carry out various functions relating to the signalling pathway in the cell, such that the cell may be induced to carry out various functions relating to the signalling pathway in the cell, such that the cell captuation of a signalling pathway in the cell, such that the cell may be induced to carry out various functions relating to the ceptically as abone marrow transplant) into a mammal to provide a source of cytotoxic effector cells that can kill cells captually as the modified cells are activated in presence of A33+ cells.
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restricted signal activation - inducing cytotoxic effector cells or cytokine production in presence of tumour cells expressing the A33 antigen, and related vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 gaagtgaagcttgtggagtctggggggggggcttagtgaagcctggagggtccctgaaactc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e-76;
0; Mismatches 34
                                                                                                                                                                                                                                          Example 3; Page 42-43; 90pp; English.
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AA062764;

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AAQ62764 RESULT

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TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                           Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; human breast carcinoma; murine anti-human carcinoma monoclonal antibody KC-4; ss.
                                                                                                                                                               181 TTAGACACTGTGCAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC
                                                                                                                                                                                                                                                                                                     caagacactgtgacgggccgattcaccatctccagagacaatgccaagaacaccctgtac
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                                                                                                                                     CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine KC-4 immunoglobulin heavy chain variable region cDNA.
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"KC-4
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93US-0129930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; human breast carcinoma; murine anti-human carcinoma monoclonal antibody KC-4; ss.
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"KC-4 VH chain (no termination codon)"
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                                                                                                                                                                                                                                                                                                                                                                                                         Murine KC-4 immunoglobulin heavy chain variable region cDNA.
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                                                Sequence 418 BP; 88 A; 94 C; 126 G; 110 T; 0 other;
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Pred. No. 4e-75;
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89.2%;
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28-SEP-1993;
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                                                                                                                             Gaps
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variable domains. The amplified cDNAs were sequenced (AAQ62788 AAQ62789). Chimeric mouse-human antibodies were constructed using human constant regions so as to produce less immunogenic polypeptides which retained the anti-human carcinoma binding specificity of KC-4.
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                                                                                                       DB 15; Length 418;
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                                                                      Sequence 418 BP; 88 A; 94 C; 126 G; 110 T; 0 other;
                                                                                                     80.9%; Score 284; DB 15; 1
llarity 89.2%; Pred. No. 4e-75;
Conservative 0; Mismatches 30;
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Best Local Simil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                           New chimeric antibodies against human parathormone related peptide(s) - useful for, e.g. treatment of hypercalcaemia and other disorders caused by malignant neoplasm(s)
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Pred. No. 5.2e-75;
0; Mismatches 34; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TACGGCAGT---TTTGCTTACTGGGGCCCAAGGGACTCTGGTCACTGTCTCTGCA
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                                                                                                                                                                                                                           Claim 52; Page 120-121; 182pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathogens or to vitamin D resistance
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89.5%;
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Matches 317; Conservative
WPI; 1998-230640/20.
                                 P-PSDB; AAW57592
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us-08-791-391a-5.rng

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Appl Appl Appl

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APPLICANT: Hamann, Philip R.
APPLICANT: Hamann, Loss
APPLICANT: Halman, Loss
APPLICANT: Hollander, Irwin
APPLICANT: Hollander, Irwin
APPLICANT: Hollect, William
APPLICANT: Tsou, Hwels, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithic Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
CORRESPONDENCE ADDRESS:
ADDRESS:
ADDRESS:
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STATE: New Jersey
COUNTR: U.S.A.
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                          US-08-553-497A-17

US-08-207-996-26

US-08-760-840A-26

US-08-760-840A-27

US-09-266-119-26

US-09-266-119-27

US-08-487-860-11

US-08-487-860-11

US-08-487-860-11

US-08-98-611A-21

US-08-398-611A-21

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FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 56, Application US/08253877C; Patent No. 5773001; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,368
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NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-2246
TELEPHONE: 201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       One Cyanamid Plaza
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SEQUENCE CHARACTERISTICS:
LENGTH: 413 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION;
US-08-253-877C-56
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US-08-253-877C-56
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Search time 87.94 Seconds (without alignments) 755.608 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17,
Sequence 17,
Sequence 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56,
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-926-789-17
US-08-926-789-17
US-08-926-789-17
US-08-177-696C-27
US-08-177-696C-27
US-08-177-696C-27
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US-08-053-171-16
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US-08-331-398A-59
US-08-331-398A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-487-860-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324599 seqs, 94655562 residues
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                                                                                                                                                                                                                          October 11, 2001, 15:14:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                US-08-791-391A-5
351
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Maximum DB seq length: 2000000000
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267.8
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Hinman, Lois

Hollander, Irwin

APPLICANT: Hollander, Irwin

APPLICANT: Hollander, Ryan

APPLICANT: Hallett, William

APPLICANT: Hallett, William

APPLICANT: Hallett, William

APPLICANT: Hallett, William

APPLICANT: Weiss, Martin J.

TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

TITLE OF INVENTION: Conjugates of Methyltrithic Antitumor

TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSE: American Home Products Corporation

STREET: One Campus Drive

CITY: Parsippany

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07054
                                                                                     TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                                                                                                      180
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 Length 413;
                                    Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY 1995
CLASSIFICATION: 530
ATTORNEY/AGBVI INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
 Score 295; DB 1;
Pred. No. 9.7e-85;
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32,368-04
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET UNBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
 84.0%;
90.0%;
Query Match
Best Local Similarity 90.0
Matches 316; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                               Length 413;
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APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                             Score 295; DB 2;
Pred. No. 9.7e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,591
FILING DATE: Herewith CLASSIFICATION: 530
PRIOR APPLICATION DATA: APPLICATION UNMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/980,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 15, Application US/08224591
; Patent No. 5856456
                                                                                                                                                                             84.0%;
90.0%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                MOLECULE TYPE: CDNA
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linear
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Best Local Similarity
Matches 316; Conserv
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                                                            ; NAME/KEY: CDS
; LOCATION: 6..4
US-08-452-164A-56
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STREET: 110
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TOPOLOGY:
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US-08-224-591-15
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                                       FEATURE:
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CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
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                                                                                                                                                                                                                                                                                                                                                                                               Score 293.6; DB 2; Length
Pred. No. 3.3e-84;
0; Mismatches 34; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                    REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/224,591
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90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker I
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessle:
                    APPLICATION NUMBER: US 0:
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           join(1..711)
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Best Local Similarity 90.2
Matches 314; Conservative
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COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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US-08-926-789-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TACGGCAGTTTTGCTTACTGGGGCCCAAGGGACTCTGGTCACTGTCTCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 GTAGTCCCGTTTGCTTACTGGGGCCAAGGACTCTGGTCACTGTCTCT 711
                                                                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                 Score 293.6; DB 2
Pred. No. 3.3e-84;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/926,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08926789
Patent No. 5990275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/224,591
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 721 base pairs TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                  83.6%;
90.2%;
                                                                                                                                                                                                                                                 Query Match 83.67
Best Local Similarity 90.23
Matches 314; Conservative
                                                                                                                                                                                join(1..711)
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: joir
US-08-224-591-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-926-789-15
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Gaps

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LENGTH: 733 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity 90.28
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(1..723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-926-789-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
CORRESPONDENCE: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TACGGCAGTITIGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTT 348
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Pred. No. 3.4e-84;
0; Mismatches 34;
        CLASSIFICATION LITERALLY
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN·1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20.NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REESENCE/DOCKET NUMBER: 99,021
REESENCE/DOCKET NUMBER: 0977.1920002/JAG
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2500
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STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.6%;
Best Local Similarity 90.2%;
Matches 314; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                LENGTH: 733 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                 join(1..723)
Herewith
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STATE: D.C.
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; LOCATION:
US-08-224-591-17
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61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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Sequence 27, Application US/07977696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Jenardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224,591
FILING DATE:
APPLICATION NUMBER: 08/002,845
FILING DATE: 1-5AN-1993
PRIOR APPLICATION DATA: 05/301
FILING DATE: 10-5AN-1993
PRIOR APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
ITELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TENCOMMUNICATION: 17:
SEQUENCE CHARACTERISTICS:
TENCOMMUNICATION: 17:
TELEPHONE: 733 hase pairs
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 293.6; DB 2;
Pred. No. 3.4e-84;
0; Mismatches 34;
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90.2%;
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APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CAPPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFTCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Anzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
                                                                                                                                                          ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS 5.0
          Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 89.2%;
Matches 321; Conservative
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: n.a.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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    for Carcinomas and Kit and Diagnostic Vaccination and Therapeutic Methods. \ensuremath{\mathrm{B1}}
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Pred. No. 3e-81;
0; Mismatches 30; Indels
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
CONFUREN: PATENTIN Release #1.0, Version #1.25
CONFRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FLING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMZEL PALO, VIVIAIN
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 96 38227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1748-6688
                                                                                ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/08129930B
Patent No. 5804187
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: n.a.
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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ilarity 89.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION: FOR TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 8: CORRESPONDENCE ADDRESS:
                                                                                                                      CITY: Los Angeles
STATE: California
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US-07-977-696C-27
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US-08-129-930B-27
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Best Local Simi
Matches 321;
                                                                                                                                                        COUNTRY:
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240 61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120 118 TCCTGTGCGCCTCTGGATTCGCTTTCAGTAGCTATGCCATGTCTTGGGTTCGCCAGTCT 177 121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTAGCACCTACTAT 180 237 238 CAAGACACTGTGACGGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTAC 297 241 CIGCAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300 301 TACGG------CAGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 351 58 GAAGTGCAGATGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTC 117 Gaps 1 GAAGTGCAGCTGGTGGAGTCTGGGGGGGGGGCTTAGTGAAGCCTGGAAGGTCCCTGAGACTC 181 TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC 6 Length 418; Score 284; DB 1; Length 41 Pred. No. 3e-81; 0; Mismatches 30; Indels

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/standard_name= "Heavy Chain
V-region of BR55-2 Antibody in pVg-1c and pVg-3c"
                   238 CTTCAAATGAGCAGTCTGAAGTCTGAGGACACAGCCATTTATTACTGTGCAAGTCACTAT 297
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Pred. No. 4.2e-77;
); Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
                                                                                                                                                                                                      Sequence 10, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INTENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
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87.1%;
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LOCATION: 1..445
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440..445
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TYPE: nucleic acid
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Best Local Similarity 87.18
Matches 311; Conservative
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MEDIUM TYPE: Floppy
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OTHER INFORMATION:
US-08-053-171-10
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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12..425
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LOCATION:
                                                                                                                                                               RESULT 10
US-08-053-171-10
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                                                                                            APPLICANT: Kris, Richard
APPLICANT: Ricca, George A.
APPLICANT: Cheadle, Christopher
APPLICANT: South, Victoria J.
ATITLE OF INVENTION: Monoclonal Antibodies Specific to Human
TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods
TITLE OF INVENTION: Employing Same
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Pred. No. 1.1e-79;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Macinicsh OPERATING SYSTEM: System 7.1 SOFTWARE: Word 5.0 (Patentin) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,761 FILING DATE: 07-UN-1995 CLASSIFFCATION: 424 PRIOR APPLICATION UMBER: US 08/086,411 FILING DATE: 29-UNN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      3: Rhone-Poulenc Rorer Inc.
500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A0207C-US
                                      Schlessinger, Joseph
Givol, David
Bellot, Francoise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: GOODMAD, ROSANDE
REGISTRATION NUMBER: 32,534
REFRENCE/DOCKET NUMBER: A020'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS: 14:
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ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: MacLitcsh
COUNTER: MacLitcsh
COUNTER: MacLitcsh
COUNTER: MacLitcsh
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Best Local Similarity 90.5%;
Matches 323; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    ADDRESSEE: Rhone-Po
STREET: 500 Arcola
CITY: Collegeville
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; LOCATION: 1..3
US-08-487-761-14
Patent No. 6217866
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                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
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TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
                                                                   CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCTACTAT 180
                                                                                                                                    TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTATAC 240
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Variable Domain of BR55-2 Murine IgG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08053171
Patent No. 5562903
GENERAL INFORTION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-54-1
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 491 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: ATCC HB 9324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
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OTHER INFORMATION:
OTHER INFORMATION:
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Thelsen, Timothy
APPLICANT: Thelsen, Timothy
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Hurle, Mark
APPLICANT: Mark
ANDRESSEE: Smithallectual Property
STREET: 709 Swedeland Road
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                                             /standard_name= "Complementarity-determining Region CDR1"
                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 282..332
OTHER INFORMATION: /standard_name=
OTHER INFORMATION: "Complementarity-determining Region CDR2"
FEATURE:
                                                                                                                                                                                                                                                                                         /standard_name=
"Complementarity-determining Region CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels
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87.1%; Pred. No. 4.4e-77;
ive 0; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-07659-1; Sequence 1, Application PC/TUS9407659; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 225..239
OTHER INFORMATION: /sta
OTHER INFORMATION: "COM
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Best Local Similarity
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STATE: CA
COUNTRY: USA
ZIP: 94662-8097
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US-08-475-000-15
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Patent No. 5811267
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSES: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.8%; Score 269.4; DB 5;
86.8%; Pred. No. 1.8e-76;
tive 0; Mismatches 41;
PatentIn Release #1.0, Version #1.25
                          APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-70L-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
                                                                                                                                                 NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REGISTRATION NUMBER: 950171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEPHONE: (610) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 86.8
Matches 310; Conservative
                 DATA
                 CURRENT APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 169
SOFTWARE:
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US-08-475-000-15
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61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
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APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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CITY: Emeryville
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,000
FILING DATE: O7-JUN-1995
CLASSIFTCATION: 424
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US-08-483-199-15
; Sequence 15, Application US/08483199
; Patent No. 5849877
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0850.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFRX: (510) 605-3542
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CHIRON CORPORATION
Floppy disk
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,508
FILING DATE: U7-JUN-1995
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0850.008
TELEPHONE: (510) 601-585
TELEFAX: (510) 601-585
TELEFAX: (510) 601-585
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86.6%;
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Best Local Similarity 86.6
Matches 309; Conservative
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US-08-484-508-15
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Pred. No. 4e-76;
0; Mismatches 42; Indels 6
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Patent No. 5948647
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: Emeryville
                                                                                                 OPERATION SISTEM: rc.DOS/mo-LOOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,199
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 0850.009
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (510) 601-2585
TELEFAX: (510) 655-3342
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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86.6%;
                                      Floppy disk
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Matches 309; Conservative
     COMPUTER READABLE FORM:
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COUNTRY: U
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; LOCATION:
US-08-483-199-15
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US-08-484-508-15
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6
      Length 357;
                                              Indels
                                              42;
Score 267.8; DB 2;
Pred. No. 4e-76;
0; Mismatches 42;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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321
1 GATATTGTGCTAACTCAGTC......GGACCAAGCTGGAAATTAAG 321
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                     1344157 segs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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em_htg_hum1:
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em_or:*
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Perfect score:
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Database :

Searched:

Sequence:

Run on:

M35667 Mouse lysoz AFL63757 Was muscu M95945 Mouse mRNA M93959 Mouse Ig ac E07933 CDNA encodi 131959 Sequence 82 I78571 Sequence 82

AX060786 MUSIGKACY AF163757 MUSCMVH MUSIGKXD E07933 I31959 I78571

AX060786 Sequence

Description

SUMMARIES

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KLEIK
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 321)
                                                                                                                                                                                                                                                                                                                                               immunoglobulin light chain; immunoglobulin-kappa; processed gene; variable region VK23.
Mouse hybridoma, cDNA to mRNA, clone 10K-106.
                                                                                                    MUSIGKACY 321 bp mRNA ROD 27-APR-1993
Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
mRNA, partial cds.
                                                                                          CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACAGGTATCAACAAAAATCA 120
                                                                                                                              CATGAGICTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC 180
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/note="lysozyme binding Ig kappa chain V23-J2 region"
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Brooks, W.B.R.
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                                                               121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                              A three-dimensional model of an anti-lysozyme antibody J. Mol. Biol. 194, 713-724 (1987) 88011212
                   Length 321;
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                    Score 321; DB 9;
Pred. No. 3.8e-99;
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                                      Mismatches
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100.0%; Pr
tive 0;
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Best Local Similarity 95.6
Matches 306; Conservative
                                      Matches 321; Conservative
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                  Query Match
Best Local Similarity
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RLIKYRSQSISGIPSRFSGSGSGTDFALSINSVETEDFGMYFCQQSGSWPHTFGGGT
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 311)
Huse, W.D. and Wu, H.
Anti--gla V7-gl(b)37 recombinant human antibodies, nucleic acids encoding same and methods of use
Patent: WO 0078815-A 7 28-DEC-2000;
Applied Molecular Evolution (US)
 Sequence 82
                                                                                                                                                                                                                                                 M.musculus
                                                                                                                                                                                                                                                                           Mouse
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/note="unnamed protein product"
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AX060786
AX060786.1 GI:12406166
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MUSANTDNAF
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MMIGLT91
MUSIGKABJ
AF139235
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AF113243
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AF139845
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AF045514
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AF139847
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286.8
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Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA. Musc musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                            1 (bases 1 to 321)
Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S.,
Co, M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="domesticus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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1. .321
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Location/Qualifiers
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79 c 77
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Matches 305; Conservative
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Mus musculus mAb 101.4.1 immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 321)
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Mertens, N.M. and Cunningham, M.W.
Direct Submission
Submitted (03-40N-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma
City, OK 73190, USA
                            AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
                                                                                                                                                             240
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            CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAATCA 120
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Pred. No. 1.5e-90;
0; Mismatches 15; Indels (
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    .321
    /organism="Mus musculus"
    /strain="BALB/c"
    /db_xref="taxon:10090"

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llarity 95.3%;
Conservative (
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AF163757
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C12P21/08,A61K39/395,C07K15/00,C12N15/13,(C12P21/08,C12R1:91); strandedness: Double; topology: Linear; hypothetical: No;
                                                                             PAT 29-SEP-1997 mouse anti-FHV-1 antibody L chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .381
/organism='Mus sp.'
1. .381
1. .antibode='variable region of mouse anti-FHV-1
antibody L
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 31)

Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y.

RNTI-FELINE HERRES VIRÜS-I RECOMBINANT ANTIBODY AND GENE FRAGMENT PRICODING THE SAME ANTIBODY

Patent: JP 1994217786-A 2 09-AUG-1994;

CHEMO SERO THERREDUT RES INST
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KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 381;
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Pred. No. 1.5e-90;
0; Mismatches 15;
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                                                                  CDNA encoding variable region of
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/organism="Mus sp."
/db_xref="taxon:10095"
a 98 c 86 g 10
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JP 1994217786-A/2
09-AUG-1994
    337 GGGACCAAGCTGGAAATAAA 356
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Best Local Similarity 95.3%;
Matches 305; Conservative
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                                                                                                                                        JP 1994217786-A/2.
Mus sp. .
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/product="immunoglobulin kappa-chain"
/product="immunoglobulin kappa-chain"
/protein_id="AaA39079.1"
/db_xref="GI:554.48"
/db_xref="GI:554.48"
/translation="GIMLEWISASRCDIVLTQSPATLSVTPGDKVSLSCRASQSISNY
/HWYQQKSHESPRLIKYVSGSISGIPSRFSGSGSGTDFTLSINSVETEDFGWYFCQQ
SNSWPHTFGSGTKLEIRRADA"
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Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus cDNA to mRNA.
Mus musculus
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Pred. No. 1.5e-90;
0; Mismatches 15; Indels
                                                                                               MUSIGKXD 370 bp mRNA ROD MOUSE IG active Kappa-chain V-region, partial cds. M93959
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    .370
    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /map="6"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="lgK"
/note="putative"
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GGGACCAAGCTGGAAATTAA 320
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/gene="IgK"
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Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelingh,K.L. and Selick,H.E.
Humanized immunoglobulins
Patent: US 5693762-A 82 02-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                      AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
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            Score 296; DB 10;
Pred. No. 1.5e-90;
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Pred. No. 1.5e-90;
0; Mismatches 15;
                                       0; Mismatches
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178626 GI:3014780
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                                                                 06-FEB-1997
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Ucuen.C.L., Schneider,W.P. and Selick,H.E.
Polynucleotides encoding improved humanized immunoglobulins
Patent: US 5693761-A 82 02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                        Length 381;
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                     Score 296; DB 10;
Pred. No. 1.5e-90;
0; Mismatches 15;
                                                                                                                                                                   Queen, C.L. and Sellok, H.E.
Humanized immunoglobulins.
Patent: US 5585089-A 82 17-DEC-1996;
Location/Qualifiers
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Sequence 82 from patent US 5693761.
178571 GI:3014725
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                                                                              5585089
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92 c 89 g
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82 from patent
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Best Local Similarity 95.3%;
Matches 305; Conservative
                                                                            Sequence 82 from pate
131959
131959.1 GI:1822750
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KEYWORDS SOURCE

REFERENCE

AUTHORS TITLE JOURNAL FEATURES

us-08-791-391a-7.rge

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241 GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGCTTCGGAGGG 300
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ASOSVSNNLHWPQQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVETED
FGMYFCOQSNSWPFTFGGGTKLBIKRADAAP"
93. .>431
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                                                                                                                                                                                                                                                                                                                                                                                                               Draft entry and computer-readable sequence [2] kindly submitted by G.Rule, 20-JUL-1988.
                                                                                                                                                       Mouse Ig rearranged kappa-chain mRNA, clone AN11K.
M19913 103332
M19913.1 GI:197033
C-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACAGGTATCAACAAAAATCA 120
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                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 431)
Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
bodies for NMR studies
Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCCAGGAGATAGCGTCAGT 60
                                                                                                                                            26-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="immunoglobulin kappa-chain"
/protein_id="AAA38888.1"
/db_xref="GI:197034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"immunoglobulin kappa-chain"
107 c 102 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_type="mature B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                        361 GGGACCAAGCTGGAAATAAA 380
                                        301 GGGACCAAGCTGGAAATTAA 320
                                                                                                                                           431 bp
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Matches 305; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi: Muridae; Murinae; Mus.
1 (bases 1 to 321)
Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S.,
Co,M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L.
                                                                                                                                                                                                                                                                                                                            Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
Mus musculus
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LOCUS AF139849 324 bp mRNA ROD 04-NOV-1999
DEFINITION Mus musculus clone 38 immunoglobulin kappa light chain variable
181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGGAGACT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                     26-JUL-1993
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es 16; Indels
                                                                                                                                                                                                                     ROD
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Fred. No. 5.2e-
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain-"BALB/C"
/sub_species-"domesticus"
/db_xref="taxon:10090"
/cell_line="MAB 33"
/cell_type="hybridoma"
1. 321
/note="putative"
a 81 c 74 g 80 t
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/organism="Mus musculus"
                                                                                                                                                                                                                  MUSCMVF 321 bp mRNA
MOUSE mRNA sequence, partial cds
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                                                             301 GGGACCAAGCTGGAAATTAA 320
                                                                                       393 GGGACCAAGCTGGAAATAAA 412
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95.0%;
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M95943.1 GI:309175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1992)
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/protein_id="Aad28632.1"
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/translation="DVLTQSPATLSVTPGDSVSLSCRASQSISSNLHWFQQKSHESP
RLLIKYASQSISGIPSRFNGSGSGTDFTLSINSVETEDFGMYFCQQSDNWPHTFGSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="immunoglobulin kappa light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamanla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 324)
Brand, F., Shannon, M., Prak, E.L., Litwin, S. and Weigert, M. Somatic mutation and light chain rearrangement generate autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice 94406777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 324)
Brard,F. and Weigert,M.
Direct Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      AF139845 324 bp mRNA ROD 04-NOV-1999
Mus musculus clone 79 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
                                                                                                                                       241 GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGACAACTGGCCTCATACGTTCGGATCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="B cell hybridoma (spontaneous fusion with SP2/0]"
    121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCCAGTCCATCTTGTGGGATCCCCTCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70. .105
/gene="lgG"
/note="CDR1; complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity determining region 3"
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                                         181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
                                                             GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/chromosome="6"
/clone="79"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IgG"
/note="variable region (VJ)"
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                                                                                                                                                                                                301 GGGACCAAGCTGGAAATTAA 320
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/gene="IgG"
/note="CDR2;
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AF139845.1 GI:4732154
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/note="CDR3;
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/gene="IgG"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukamanlaia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
                                                                                                                                                                                                                                                                                             2 (bases 1 to 324)
Brand, F. and Weigert, M.
Brand, F. and Weigert, M.
Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
1 . 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="38"
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sp2/n)"
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Pred. No. 5.2e-90;
0; Mismatches 16;
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region Vk23 (IgG) mRNA, partial cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="spleen"
<1. .>324
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287. .324
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Best Local Similarity 95.0%;
Matches 304; Conservative
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/gene="IgG"
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Vk23"
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Gilbert,D., Lopez,B., Parain,J., Koutouzov,S. and Tron,F.
Overlap of the anti-cardiolipin and anti-nucleosome responses of the (NZW X BXSB)FI mouse strain: a new pattern of cross-reactivity for lupus-related autoantibodies
Eur. J. Immunol. 30 (11), 3271-3280 (2000)
2 (bases 1 to 321)
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AJ277215 GI:7529622 GI:7529622 immunoglobulin light chain; monoclonal antibody; variable region.
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/gene="IgG"
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Pred. No. 1.9e-89;
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                                                                    /protein_id="AAD28633.1"
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265. .291
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287. .324
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Best Local Similarity 94.7%;
Matches 303; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 324)

Brard.F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.

Somatic mutation and light chain rearrangement generate

autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice

J. Exp. Med. 190 (5), 691-704 (1999)
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2 (bases 1 to 324)
2 (bases 1 to 324)
Brardf F. and Welgert, M.
Direct Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF139846 324 bp mRNA ROD 04-NOV-1999
Mus musculus clone 15 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
AF139846 GI:4732156
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SP2/0)"
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                                                                                                         DB 94; Length 324;
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/db_xref="taxon:10090"
/chromosome="6"
                                                                                                                                           Indels
                                                                                                    Score 292.8; DB 94;
Pred. No. 1.9e-89;
0; Mismatches 17;
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               /note="Jk2'"
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Best Local Similarity 94.7%;
Matches 303; Conservative
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/gene="IgG"
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RLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQSNNWPLFFGAGT
KLELK"
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Gilbert, D.
Direct Submission
Submitted (30-MAR-2000) Gilbert D., Immunology, U519 INSERM, 22 bd
Gambetta, 76183 ROUEN cedex, FRANCE
Location/Qualifiers
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/note="anti-cardiolipin monoclonal antibody"
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/organism="Mus musculus"
/organism="NuZWBXBSB]F1"
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/clone="1G11"
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BF579007 949 bp mRNA EST 12-DEC-2000 602096124F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4216180 5',
            Tissue Procurent: Jeffrey B. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Prayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: The J.M.A.G.B. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.lln.gov f column: 11

High. quality sequence stop: 714.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                    /strain="FVB/N"
/db_xref="taxon:10090"
Email: cgapbs-r@mail.nih.gov
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CDNA clone IMAGE:4219402 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                 Description
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602099743F1 NCI_CGAP_Co24 Mus musculus
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Contact: Robert Strausberg, Ph.D.
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BC569760
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AW405309
AW404697
AW404506
AW405025
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AW404726
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169.4
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DEFINITION

RESULT BF582153

ACCESSION

VERSION KEYWORDS SOURCE

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

ORGANISM

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125 197 185 257 245 317 302 376

137

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Tissue Procurement: Gilbert Smith, Ph.D.
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                                                                                                                                                                                                              // Organism="Mus musculus"
/strain="FyBN"
/strain="FyBN"
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/ste_2: SalI: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheriat; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 624)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GICTCCAAGGCTTCTCAACGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCCAGGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 CAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACTGAAGA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 TTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGGGGGAC 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 TGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCCAGGAGATAGCGTCAGTCTTTC 65
        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 730.
Location/Qualifiers
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Pred. No. 4.7e-71;
0; Mismatches 29; Indels
lissue Procurement: Jeffrey E. Green, M.D.
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BE306691.1 GI:9160297
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90.4%;
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Best Local Similarity 90.45
Matches 284; Conservative
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 849)
11 (bases 1 to 849)
12 (bases 1 to 849)
13 (bases 1 to 849)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 CATGGGACTCCAAGGCTTCTCATCAAGTATGCACCTGATCCCATCTGGGATCCCTCC 238
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clans Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov g column: 20
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Location/Qualifiers
1. .624
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AGGTTCACTGGCGAGTGGGATCAGGGACAGATTACACTCTCAGTATCAACAGTGTAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233.6; DB 166; Length 624;
Pred. No. 4.8e-64;
0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 83.1%;
Matches 266; Conservative
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TITLE
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_1: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homoo sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 434)
INH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Thoryte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.n column: 08
High quality sequence stop: 575.
Location/Qualifiers
1. 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW406486 434 bp mRNA EST 16-FEB-2000 UI-HF-BLO-acr-f-12-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060238 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 204; DB 166; Length 708; Pred. No. 1.6e-54; 0; Mismatches 65; Indels 1:
                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/clone="InAGE:3489991"
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/dev_stage="tumor, gross tissue"
/lab_host="DH10B"
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79.48;
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Best Local Similarity 79.4:
Matches 254; Conservative
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                                                                                                                                                                                                                                                                                                                                                  1..849
/organism="Mus musculus"
/strain="FVBus musculus"
/strain="FVBus musculus"
/db_xref="taxon:10090"
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/note="Organ: colon: Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Rverage insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                              Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov

Plate: LLAM9815 row: column: 14

High quality sequence stop: 627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 223.8; DB 150; Length 849;
Pred. No. 7.3e-61;
0; Mismatches 42; Indels 2:
          3mail: cgapbs-r@mail.nih.gov
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Best Local Similarity 86.0%;
Matches 271; Conservative
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Conference: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nlh.gov
   Tissue Procurement: CLONTECH Laboratories, Inc.
   CDNA Library Preparation: CLONTECH Laboratories, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.lln.gov
   Plate: LLCM1566 row: e column: 18
   High quality sequence stop: 738.
   Location/Qualifiers
   I. 9466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CTTTCCTGCCAGGCCAGCCAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AGGITCAGIGGCAGIGGATCAGGGACAGAITICGCICTCAGIAICAACAGIGIGGAGACI 240
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW405183 519 bp mRNA EST 16-FEB-2000 UI-HF-BL0-acb-b-10-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058506 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GGGACCAAGCTGGAAATTAA 320
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                      Unpublished (1999)
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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
            Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward
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602590367F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4717049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 194.4; DB 115; Length 434; Pred. No. 1.6e-51; 0; Mismatches 76; Indels 0;
Contact: Robert Strausberg, Ph.D.
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ilarity 75.9%;
Conservative
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TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                E 1 (bases 1 to 398)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov

Email: capabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

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CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

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www-bio.llnl.gov/bbrp/image/image.html

Seq primer: Mi3 Forward.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
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UI-HF-BLO-acd-b-04-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058518 5', mRNA sequence.
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Best Local Similarity 74.4%;
Matches 238; Conservative
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                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.infi.gov
Exall: cgapbs-rémail.infi.gov
Exco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbry/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
Chordata, Craniata; Vertebrata, Euteleostomi, Primates; Catarrhini; Hominidae; Homo.
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                                   Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 519)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 74.7%; Pred. No. 3.3e-50;
Matches 239; Conservative 0; Mismatches 81; Indels
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BASE COUNT ORIGIN

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Gaps

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283

AW405309 LOCUS DEFINITION

RESULT

ACCESSION VERSION KEYWORDS

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IMAGE:3058065 5', mRNA sequence.
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les 237; Conserv
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Matches
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KEYWORDS
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                                                                                     Homo sapiens but a chordata; Craniata; Vertebrata; Buteleostomi; Bukrayota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 465)
NTH-MGC http://mgc.nci.nih.gov/.
NTH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                            Contact: Rober Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Enc NI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llni.gov/bbry/image.image.html
Seq primer: M13 Forward.
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   GI:6923754
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                                                                                                                                                                                 REFERENCE
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JOURNAL
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(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. tibrary preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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In the McC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
In the McC http://mgc.nci.nih.gov/
In the McC http://mgc.nci.nih.gov/
Email: capabs-rémail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Standt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: MI3 Forward.
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%; Score 187.2; DB 115; Length 468; 74.1%; Pred. No. 3.4e-49; Live 0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
AW404506.1 GI:6923563
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                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nin.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
Seq primer: Ml3 Forward.
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 468) WIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                             AW405643 468 bp mRNA EST 16-FEB-2000
UI-HF-BLO-abs-f-05-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057561 5', mRNA sequence.
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0; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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1. .468
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73.8%;
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                                                                                                        DEFINITION
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COMMENT
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(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Libzary preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW405025 385 bp mRNA EST 16-FEB-2000 UI-HF-BL0-abx-e-03-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058252 5', mRNA sequence.

AW405025 IG:6924082
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 TCCTGCAGGGCCAGTCAGAGTGTTCGCAGCTACTTAGCCTGGTACCAGGAAACCTGGC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 GATTTTGGAATGTATTTCTGTCAACAGAGTGGCCAGGCTGGCCTCACACGTTCGGAGGGGGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGACACCAGGAGATAGCGTCAGTCTT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.9%; Score 185.8; DB 115; Length 385; ilarity 74.1%; Pred. No. 8.9e-49; Conservative 0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Bukaryota; Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 482)
Yang, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
Oian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Ghen, J.,
Chen, Z. and Han, Z.
Unpublished (2000)
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                                                                                                                                                                                                                                                                                              Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgebpc.sh.cn
This clone is available at CHGC in Shanghai.
                                                           AV733856 482 bp mRNA EST 17\text{-}OCT\text{-}2000 AV733856 cdA Homo sapiens cDNA clone cdABAH01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
152 c 122 g 111 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.8%; Score 185.6; DB 32; Length 73.8%; Pred. No. 1.1e-48; Live 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pheochromocytoma"
/dev_stage="Adult"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cdABAH01"
/clone_lib="cdA"
                                                                                                       AV733856.1 GI:10851401
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
BG536848 1015 bp mRNA EST 03-APR-2001 602566386F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4691085 5',
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Best Local Similarity 73.8%;
Matches 236; Conservative 0
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Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; anglogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.
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/product= "LM609 antibody light chain variable region"
/note= "partial sequence, no start or stop codon given"
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               AAE28199
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AAT42033
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(IXSY-) IXSYS INC.
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Sequence of mouse
Murine CMV5 antibo
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Mouse anti-verotox
Murine vitronectin
EGF receptor chime
                                                                                                                              (without alignments)
1134.570 Million cell updates/sec
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Vitaxin light chai
LM609 antibody lig
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                                                                                                                                                                                                            GATATTGTGCTAACTCAGTC......GGACCAAGCTGGAAATTAAG
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           730101 seqs, 313950809 residues
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                                                                                                             October 11, 2001, 15:12:37
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Listing first 45 summaries
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AAQ64167
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    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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Plasmid pww152-225 Plasmid pSw202-225 Plasmid pw238-225 Plasmid pw538-225 Plasmid pw538-225 DNA encoding the 1

Insert coding for Anti-gp54 MAb 48-1 Monocional antibod Fv(TU25). Homo sa

scrv comprising

Light chain variab Light chain variab B-B10 MAb L chain Anti-gp54 MAb 48-1

Humanised anti-alp Vitronectin alpha-Humanised antibody

Light chain coding Humanised anti-ver

Expression vector

Mouse monoclonal a

Human secreted exp DNA encoding light

H. pylori beta-ure Anti-IL2R-beta ant CDNA encoding kapp Humanised antibody

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Jk gene segment. Humanised anti-alp Monoclonal antibod

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                                                                                                                                                                                                                                                                          This sequence encodes the LM609 antibody variable light chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin—mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non )immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psorlasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
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                                                                                                                  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 321; DB 19; 100.0%; Pred. No. 3e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody LM609 light chain variable region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                    Claim 40; Fig 2b; 129pp; English.
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                                                                                                                                                                                        anglogenesis or restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 321; Conservative
    Huse WD
                                              WPI; 1998-437472/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                   P-PSDB; AAW75004
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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGAGICTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of cancer disorders such as tumours and Kaposi's sarcomal, retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 321; DB 22;
100.0%; Pred. No. 3e-95;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                             (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of mouse V-kappa showing anti-FHV-1 antibody CDRs 1, 2 and
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23-JUN-2000; 2000WO-US17454.
                                                        99US-0339922
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Best Local Similarity 100.
Matches 321; Conservative
                                                                                                                                                                                                                          WPI; 2001-050110/06.
                                                                                                                                                                        Wu H;
                                                                                                                                                                                                                                                                                                                                                                           osteoporosis -
                                                     24 -JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The inventors claim a monoclonal antibody against feline herpes virus (FHV-1). They also claim a recombinant antibody against FHV-1 and fragments of VH and VL CDR1, CDR2 and CDR3. The antbodies are used in the detection, treatment and prevention of FHV-1. The sequences of the CDRs in the VH of the recombinant anti-FHV-1 antibody are given in AAR54092. The sequences of the CDRs in the VL cthe recombinant anti-FHV-1 antibody are given in AAR54093. These CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC
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0
                                                                                                                                                                                                                                                                                                                                                                                                    Feline monoclonal antibody and recombinant antibodies specific for {\sf FHV-1} - for detection, treatment and prevention of {\sf FHV-1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 296; DB 15; Length 381; llarity 95.3%; Pred. No. 4.7e-87; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
            Feline herpes virus; FHV-1; monoclonal antibody; CDR; complementarity determining region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       Maeda H, Nishiyama K, Tokiyoshi S;
                                                                                                                                                                                                                                                                                                            SERO THERAPEUTIC RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 18-19; 53pp; Japanese.
                                                                           Location/Qualifiers
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/label= MJK124
                                                                                                                                        /label= MKL104
385..429
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P-PSDB; AAR54093.
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nes 305; Conserv
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                                                                                                                 misc_feature
                                                   Mus musculus
                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                           25-NOV-1993;
                                                                                                                                                                                                                                                                                    28-NOV-1992;
                                                                                                                                                                                                                                09-JUN-1994
                                                                                                                                                                                                                                                                                                                                       Kimachi K,
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Matches
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The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections and myeloid leukaemia. The present sequence is an antibody cDNA used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;
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Pred. No. 4.7e-87;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                               Murine CMV5 antibody light chain cDNA SEQ ID NO:
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                                    361 gggaccaagctggagctgaa 380
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89US-0310252.
90US-0590274.
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95.3%;
                                                                                                                                                                                                                        CDNA; 381
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GGGACCAAGCTGGAAATTAA
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Best Local Similarity 95.3
Matches 305; Conservative
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                                                                                                                                                                                                                    AAF58747 standard;
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28-SEP-1990;
19-DEC-1990;
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AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT

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ctttcctgcagggccagccaaagtattagcaaccaactactactgtatcaacaaaaatca 126

29

GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300

GGGACCAAGCTGGAAATTAA 320

AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding the FG chain of antibody MAK33 were used to transform E.coli DSM 3689 and the resulting cells grown to form inclusion bodies. After the final renaturation step an 18% yield of blologically active protein was
CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC 180
                      240
                                             240
                                                                                          GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                      SS
             AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
                                                                                                                                                                                                                                                                                                             Antibody MAK33; kappa chain; plasmid pBT111; activated antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activated antibody prodn. from recombinant procaryotic cells by solubilisation under reducing conditions, then oxidative renaturation, carried out at low protein concn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;
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                                                                                                                                                                                                                                                                                       Plasmid pBT111 encoding antibody MAK33 kappa chain.
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/*tag= a
/product= kappa chain of MAK33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rudolph R, Buchner J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-156813/21
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for treating Verotoxin
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                                                                                                                                                                  Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1; monoclonal antibody; light chain; mouse; humanised antibody; Escherichia coli; VTEC; infection; haemolytic uraemic syndrome; therapy; ss.
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/transl_except= (pos:184..186, aa:Lys)
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                                                                                                                                             Mouse anti-verotoxin II antibody VTm1-1 VL cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized antibody binding to verotoxin II producing E. coli
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1..60
/*tag= a
58..381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1b; 59pp; English.
                                                                BP.
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gggaccaagctggagctgaa 326
                                                                AAZ35242 standard; cDNA; 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Imaizumi
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                                                                                                                   13-MAR-2000
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                                                                                                                                                                                                                                       Mus musculus
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                                                                                         AAZ35242;
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Gaps

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CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAATCA 120

1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60

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heavy and light chain frameworks, provided that at least 1 position selected from L49, H29, H30, H49 and H98 is occupied by the amino acid at the equivalent position of the MuvTmi-1 antibody heavy or light chain variable region framework. Such humanized antibodies (see AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times that of MuVTmi-1. They are used for treating a patient suffering from, or at risk of, the toxic effects from VT2 (claimed), especially for treating verotoxin producing Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised antibody; monoclonal antibody; MAb; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 aggitcagiggcagiggatcaggacagatitcacitcicagiatcaacagigigaaaci
                                                                                                                                                                                                                                                                1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                    CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; anglogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                      DB 21; Length 381;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine vitronectin alpha-v beta-3 receptor MAb VL cDNA.
                                                                                                                                                     Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;
                                                                                                                                                                                                     Score 283.2; DB 2
Pred. No. 7.1e-83;
                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 gggaccaagctggagctgaa 380
                                                                                                                                                                                                     88.2%;
92.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV71798 standard; cDNA; 324
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                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                Best Local Similarity
Matches 297; Conserv
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cee AAW84094) of the anti-human alphav beta-3 vitronectin receptor murine monoclonal antibody D12. It was obtained from hybridoma to the monoclonal antibody D12. It was obtained from hybridoma to the monoclonal antibody D12. It was obtained from hybridoma to the manoclonal antibody D12. It was obtained from hybridoma to the monoclonal antibody D12. It was obtained by the man by RT-PCR using mouse kappe and N-terminal-based primers (see AAV71808-09). A heavy chain variable region clone (see AAV71797) has also been identified. D12 VH and VL show sequence similarity to Kabat VK subgroup III (see AAW84098) were constructed by combining the framework regions of the chaman variable sequences with complementarity determining regions of D12 (keeping some preferred murine framework residues). The humanised antibodies are specifically reactive with the human alpha-v beta-3 protein receptor and capable of neutralising the receptor. They can be used for passive immunotherapy of a disorder disorders or anglogenic-related disorders, such as angiogenesis disorders or anglogenic-related disorders, such as angiogenesis createnosis, chronic inflammatory disorders, macular degeneration, resumatoid arthritis and cancer, e.g. solid tumour metastasis, and disacases where bone resorption is associated with pathology such as consequenced by bone metastasis, bone closs due to immobilisation or sex hormone deficiency. They can also the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used for targeted drug therapy, and for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gacattgtgctgactcagtctccagccacctgtctgtgactccaggagatagcgtcagt
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                                                                                                                                                                                                                                                       This cDNA sequence codes for the light chain variable region (VL
                                                                   New anti alpha_v beta_3 vitronectin receptor antibodies - used immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 324;
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Pred. No. 7.4e-82;
0; Mismatches 25;
                                                                                                                                                                                                    Example 13; Page 59-60; 97pp; English.
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92.2%;
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                        P-PSDB; AAW84094
                                                                                                                                                      osteoporosis
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AAV49821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A cDNA clone (AAT33446) codes for the light chain variable region (V (AAM00241) of the epidermal growth factor receptor (EGF-N)-specific mouse-human chimeric antibody chwints. WH and VL chain sequences were obtd. by PCR amplification of RNA from murine Mint5 hybridoma DSM ACC2150 and fused to human C-gammal and CK genes. Constructs were expressed in CHO cell transfectants. chwint5 shows lower immunogenicity than Mint5 when administered to humans. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine/human chimeric monoclonal antibody, chMint5 specific for EGF-R - shows a lower immunogenicity when administered to humans
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used in diagnostic assays or used to produce immunotoxins or immunocytokines useful for tumour therapy.
                                                       chMint5;
                                                                     therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                          De Santis R, Di Massimo AM;
                                                    Mouse-human chimeric antibody; monoclonal antibody; epidermal growth factor receptor; BGF-R; diagnosis; immunotoxin; immunocytokine; tumour; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
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Pred. No. 9.1e-80;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 324 BP; 85 A; 83 C; 78 G; 78 T; 0 other;
                                                                                                                                                               /*tag= a
/note= "primer-derived sequence"
                                                                                                                                                                                                          /*tag= b
/note= "primer-derived sequence"
                           chimeric MAb chMint5 VL chain cDNA
                                                                                                                                                                                                                                                                                                                                                              (ITUY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 17; 28pp; English.
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Best Local Similarity 90.9%;
Matches 291; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Colnaghi MI,
(first entry)
                                                                                                                                                                                          301..324
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                           EGF receptor
                                                                                                            Mus musculus
                                                                                                                                                  misc_feature
                                                                                                                                                                                             misc_feature
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22-NOV-1996
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Vitaxin, antibody, variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "vitaxin antibody light chain variable region" /note= "partial sequence, no start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the vitaxin antibody variable light chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically anglogenesis and restenosis (but also e.g. (non-)immune finflammantion, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the contain the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 5.2e-78;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vitaxin antibody light chain variable region DNA.
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89.7%;
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/product= '
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                                                                                                                                                                                                                                                             301 gggaccaagctggagatcaa
                                                                                                                                                               GGGACCAAGCTGGAAATTAA
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Matches 288; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9833919-A2
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Sequence 321 BP; 78 A; 93 C;
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P-PSDB; AAW76006.
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                                           Similarity
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                                                     288;
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                               Query Match
Best Local
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                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of anglogenesis, inflammatory diseases e.g. psorlasis, cancers and
                                                                                   180
                                                                                               121 ggtcaagccccaaggcttctcatcaagtatcgttcccagtccatctctgggatcccgcc 180
                                                                                                                                                   240
                                                                                                                                                                       GAAGATTTTGGAATGTATTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                         CITICCTGCCAGGCCAGGCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAATCA 120
                                                                                                                                                                                             gaagattttgcagtctattactgtcaacagagtggcagctggcctcacacgttcggaggg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alphavbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), diseases (such as sasociated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumnours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments in the diagnosis and treatment of
                                                    GATAITGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT
                                                                                   CATGAGTCTCCAAGGCTTCTCAACTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC
                    gagattgtgctaactcagtctccagccacctgtctctcagcccaggagaaagggcgact
                                                                                                                                                                                                                                                                                                                                                                                   grafted antibody; alphaVbeta_3 integrin; angiogenesis; natory; cancer; retina; restenosis; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                              Vitaxin light chain variable region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 132pp; English.
                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                              301 gggaccaaggtggaaattaag 321
                                                                                                                                                                                                                   301 GGGACCAAGCTGGAAATTAAG 321
                                                                                                                                                                                                                                                                                               DNA; 321
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                                                                                                                                                                                                                                                                                            AAF28176 standard;
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                                                                                                                                                                                                                                                                                                                                                                                              inflammatory;
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                                                                                                                                                                                                                                                                                                                                         03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2000
                                                                                                                                                                                                                                                                                                                   AAF28176;
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Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; anglogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "partial sequence, no start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "LM609 grafted antibody light chain variable
                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                               61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
                                                                                                                      121 ggtcaagccccaaggcttctcatcaagtatcgttcccagtccatctctgggatcccgcc
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                                                                                                                                                                                                                                                             121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCAATCTCTGGGATCCCCTCC
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              Length 321;
                                                         Indels
Score 268.2; DB 22;
Pred. No. 5.2e-78;
                                                      0; Mismatches
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                83.68;
89.78;
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tumour; infection; depression; psoriasis;

WO200021991-A1 Homo sapiens.

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This sequence encodes a LM609 grafted antibody variable light chain alphavoberata and can be used to inhibit binding of alphavobeta on a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetLc retinopathy, neovascular glaucoma, cancer, psorlasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are sultable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
                                                                                                  Claim 24; Fig 7; 129pp; English.
                                                      anglogenesis or restenosis
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Collins-Racie LA,

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MCCOY JM,

Jacobs

(GEMY) GENETICS INST INC.

99WO-US24206 98US-0104436

15-OCT-1999; 20-APR-2000

> Gaps ö DB 19; Length 321; Indels 34; 82.8%; Score 265.8; DB 1 llarity 88.8%; Pred. No. 3.2e-77; Conservative 2; Mismatches 34 Similarity Matches 285; Query Match Best Local S

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240
                                                    CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
                                                                            61 ctttcctgccaggccaggccaaagtattagcaaccacctacactggtatcaacaaaggcct 120
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                       1 gagattgtgctaactcagtctccagccacctgtctctcagcccaggagaaagggcgact 60
GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGACACCAGGAGATAGCGTCAGT
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Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; inmunomodulatory; haemostetic; chemokinetic; analgasic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; autoimune disorder; neuroprotective; notropic; antipsoriatic; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilla; thrombosis; inflammatory disorder; Crohn's disease; Human secreted expressed sequence tag SEQ ID NO:921. ВЪ AAA44346 standard; cDNA; 651 (first entry) 21-AUG-2000 AAA44346; AAA44346

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remains to gravity to represent special control of activities depending on the tissues cheek series a range of activities depending on the tissues they were isolated from human, mouse, chicken and rate tissues cheek were isolated from the activities include:

chemotactic; proliferative; immunomdulatory; haematopoietic;

chemotactic; analgesic; haemostatic; thrombolytic; antiinflammatory;

chemotactic; antibacterial; antifuncar; osteopathic; neuroprotective;

antiasthmatic; vulnerary; antiloger; osteopathic; neuroprotective;

nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;

carticonvulsant; and antidepressant. The sESTS can be used for gene therapy and in vaccines. The sESTS are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA and enclecules which correspond to the sESTS. Proteins encoded by the sESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (crom's Alascase), tumours, bacterial, fungal or viral infections, depression and soriasis. AAA45916 to AAA4591 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA43426 to AAA45925 represent specifically claimed secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 651 BP; 174 A; 166 C; 151 G; 160 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 440; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                           Bowman MR;
                                                                                                                                                                                                                                                                                                                                                           Treacy M,
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                                                                                                                                                                                                                                                                                                                                                           Merberg D,
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Gaps ö DB 21; Length 651; 34; Indels Score 265.6; DB 2 Pred. No. 4.9e-77; 0; Mismatches 34 82.7%; Matches 286; Conservative Similarity Query Match Local

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241 GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300

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Expression vector of light chain of chimeric anti-CD40 antibody chi22.
    ggtcaagccccaaggcttctcatcnnntatcgttcccagtccatctctgggatccccgcc 180
                                                                                              GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                     Light chain variable region; chimeric antibody; anti-CD40 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                    chi220; humoral immune response; T cell dependent antigen;
collagen induced arthritis; transplant induced rejection;
T cell mediated disorder; autoimmune disease; inflammatory disease;
transplantation; ss.
                                  AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
                                                   AAZ10202 standard; DNA; 8858 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                            GGGACCAAGCTGGAAATTAAG 321
                                                                                                                                                                                            gggaccaaggtggaaattaag 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aruffo AA, Bajorath
Huse WD, Siadak AW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527408/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9942075-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-1999;
                                                                                                                                                                                                                                                                                                                                      01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999.
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                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(Y)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -
The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                    LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ds.
                                                                                                                                                                                                                                                      DNA encoding light chain variable region of LM609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 7; 132pp; English.
                                                                                                                                                          BP
                                           AAF28199 standard; DNA; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000WO-US17454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0339922
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-050110/06.
                                                                                                                                                                                                                                                                                                                                                                  WO200078815-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis
                                                                                                                                                                                                                      03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000.
                                                                                                                                                                                        AAF28199;
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                                            301
                                                                          394
                                                                                                                           RESULT 1
AAF28199
ID AAF2
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The present sequence represents an expression vector for expressing the light chain of a chimeric anti-CD40 antibody designated chi220. The antibodies are effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic anti-inflammatory properties. The antibodies have wide therapeutic transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases,
Antibody that binds human CD40, for treating T cell mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;
                                                                                                                                                                        Claim 18; Fig 14A-C; 77pp; English.
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Gaps

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Indels

36;

0; Mismatches

Conservative

Similarity

Query Match Best Local Simi Matches 285;

Length 321;

Score 265.2; DB 22; Pred. No. 5e-77;

82.6%; 88.8%;

5e-77;

CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC 180

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1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60

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Hollenbaugh

LJ, m. Wu H;

J, Berry KK, Harris LJ Thorne BA, Watkins JD,

/*tag= a /note= "no termination sequence"

99WO-US02949. 98US-0026291.

Location/Qualifiers 1065..1388

(first entry)

immunospecific agent for treating autoimmune diseases and preventing

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                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; human; heavy chain; variable region; light chain; MAb; 4-1BB; tumour necrosis factor receptor; membrane protein; accessory molecule; r-cell; antigen-presenting cell; immune response; rheumatoid arthritis; immunosuppressive agent; autoimmune disease; rejection response; therapy; organ transplantation; ss.
                                                                                                           1184
                                                                                                                                                     1244
                                                                                                                                                                                                 1304
                                                                                                                                                                                                                                  /*tag= b
/note= "constant region (encoded protein not given in
specification)"
                                                                                      120
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                                           9
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "claimed light chain variable region coding sequence"
                                                                                                                                                   1 GATATIGIGCIAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT
                                                                                      CTTICCTGCCAGGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA
                                                                                                           ctttcctgcagggccagccagagtattagcgactacttacactggtatcaacaaaaatca
                                                                                                                                                                                      CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC
                                                                                                                                                                            AGGTTCAGTGGCAGTGGATCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
                                                                                                                                                                                                                     GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
Length 8858;
                       ó
                                                                                                                                                                                                                                                                                                                                                                                                             Light chain coding sequence of monoclonal antibody 4B4-1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody specific for human 4-1BB - useful as
  DB 20;
           .8e-74;
                       0; Mismatches
  Score 259.2;
Pred. No. 1.8
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                                                                                                                                                                                                                                                                                      1365 ggcaccaagctggaaatcaa 1384
 80.7%;
88.1%;
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                                                                                                                                                                                                                                                                                                                                           AAT38510 standard; DNA; 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95KR-0008176
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P-PSDB; AAW04333.
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            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
misc_feature
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             Local Simi
nes 282;
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                                                                                                                                                                                                                                                                                                                                                                  AAT38510;
  Query Match
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completed: October 11, 2001, 15:12:39

Search completed: (Job time: 6471 sec

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                                                                                 AAT38509 and AAT38510 represent the coding sequences for the variable regions of the heavy and light chains of the antibody of the invention. This sequence is stated in the specification as being 372 bp in length, but only comprises 363 bp. The antibody of the invention (designated BAB-1-1) is a monoclonal antibody (MAb) specific for human 4-IBB. 4-IBB encodes a member of the tumour necrosis factor receptor family of integral membrane proteins. 4-IBB is an accessory molecule expressed on the surface of T-cells in the initial stage of activation. The accessory antigen-presenting cell bind to the corresponding ligand on the antigen-presenting cell and this accelerates the activation of the T- and antigen-presenting cells, thereby promoting various immune responses. The MAb is specific for human 4-IBB, which is selectively expressed on activated T-cells. The MAb is useful as an immunosuppressive agent. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 catgagicticcaaggeticticateaaataigeticeeaaiceateitgggaiceeeiee 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 gaagatgttggagtgtattactgtcaagatggtcacagctttcctccgacgttcggtgga 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
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                                                                                                                                                                                                                                                                                                                                             arthritis, and for preventing rejection response after organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 363 BP; 91 A; 102 C; 79 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 256; DB 17;
Pred. No. 5.3e-74;
0; Mismatches 40;
                                                   Claim 4; Fig 3a; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.8%;
Best Local Similarity 87.5%;
Matches 280; Conservative (
                   organ transplant rejection
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                                                                                                                                                                                                                                                                              Sequence 82, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLEI, Nicholas F.
APPLICANT: SELICK, Harolle L.
APPLICANT: SILOK, Harolle E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CIEW
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAPPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
COMPUTER: LIBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/590,274
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTONEY/AGENT INFORMATION:
NAME: SMICH, WIlliam M
RAME: SMICH, William M
REGISTRATION NUMBER: 30,223
        US-09-042-353-41

US-09-042-353-41

US-09-049-672A-19

US-08-09-74-201

US-08-09-762-180

US-09-042-353-43

US-09-240-274-107

US-09-240-274-107

US-09-240-274-107

US-09-240-274-107

US-09-240-274-109

US-09-240-274-109

US-09-240-274-109

US-09-240-274-109

US-09-240-274-109

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US-09-240-274-109

US-09-240-274-109

US-08-378-939-31
                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11823-002600 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STREET: 379 Lytton
CITY: Palo Alto
STATE: California
 ZIP: 94301
                                                                                                                                                                                                                                                           RESULT 1
US-07-634-278-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
174.8
174.8
168.4
168.4
168.4
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168.4
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165.2
165.2
163.6
163.6
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161.6
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                                                                                        (without alignments)
591.027 Million cell updates/sec
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Sequence 82, Appl
Sequence 82, Appl
Sequence 3, Appli
Patent No. 5453363
Sequence 13, Appl
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Sequence 3, Al
Sequence 3, Al
Sequence 3, Al
Sequence 3, Al
Sequence 7, Al
Sequence 7, Al
Sequence 7, Al
Sequence 1, Al
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                                                                           ; Search time 87.94 Seconds
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1 GATATTGTGCTAACTCAGTC......GGACCAAGCTGGAAATTAAG
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-192-861A-2
US-08-232-081B-35
US-08-232-081B-36
US-08-053-131-178
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                                                                                                                                                                                                    324599 segs, 94655562 residues
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                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           October 11, 2001, 15:14:14
                                                      - nucleic search, using sw model
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                                                                                                                                                                                                                                                length: 0
length: 2000000000
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Match Length
                                                                                                                    Title:
Perfect score:
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                                                                                                                               DB 1; Length 381;
                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 82, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHREIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA.
FILLING DATE: US/08/477,728
FILLING DATE: 07-UUN-1995
                                                                                                                             Score 296; DB 1
Pred. No. 2e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
                                                                                                                                                             0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             92.2%;
95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGACCAAGCTGGAAATTAA 320
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TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                              Best Local Similarity
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                                            NAME/KEY:
COCATION:
US-07-634-278-82
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                                                                                                                               Query Match
                               FEATURE
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61 CTTTCCTGCCAGGCCAACCAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
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Fatent No. 5693761
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TILLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 296; DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                              NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
US 07/290,975
                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GGGACCAAGCTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.2%;
                    FILING DATE: 28-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 95.3
Matches 305; Conservative
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-477-728-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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US-08-474-040-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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61 GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
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Pred. No. 2e-89;
0; Mismatches 15; Indels
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: CALLINGLE, Nicholas F.
APPLICANT: CAELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HARONED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT/APPLICATION DATA:
                                                                                                                                                                                                                                                                      3: Townsend and Townsend and Crew 379 Lytton Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/487,200
CLASSIFICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1955
CLASSIFICATION: 474
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/30,975
FILING DATE: 13-EB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
RECISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-00261
FILING DATE: 3-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
RECISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-00261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 95.3%;
Matches 305; Conservative
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    94301
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; LOCATION:
US-08-487-200-82
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                         STREET:
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                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: US-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 296; DB 1
Pred. No. 2e-89;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M
REGISTRATION UNDBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 82:
                                                                                                                                                          FILING DATE: 07-UN-1995
CLASSIFICATION: 536
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FRICK APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
WANNEY CARRETTED TO THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE DATA OF THE
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Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GGGACCAAGCTGGAAATAAA 380
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Best Local Similarity 95.3%;
Matches 305; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-08-474-040-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-487-200-82
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APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
                                                                                                                                                                                             CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
                                        1 GATATTGTGCTAACTCCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60
                                                                                                                                                                                                                                                                             AGGTTCAGTGGCAGTGGATCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
                                                                                                                                                                                                                                                                                                                                                      241 GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
    15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FLILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08436463 Patent No. 5760185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: K1
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GGGACCAAGCTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 424 base pairs
nucleic acid
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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: USA
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    Matches 305;
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US-08-436-463-3
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                                  241 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
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                                                                                                                                                                                                                                                                                                           APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, Wicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HAROWED HUMANIZED IMMUNOGLOBLINS
NUMBER OF INVENTION: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 296; DB 4 Pred. No. 2e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTARION UNBRER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICE STITUTION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      Sequence 82, Application US/08484537 Patent No. 6180370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                    361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                GGGACCAAGCTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%;
95.3%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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; LOCATION:
US-08-484-537-82
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247 gaagattttggaatgtatttctgtcaacagagtaacagctggcctctcacgttcggtgct 306
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                                                          GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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                                                                                                                                                                                                                                                                                                                              APPLICANT: KANG, Chang-Yuil
APPLICANT: KIM, Joong-Gon
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE 3.1
ADDRESSE: KANG, Chang-Yuil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 151-057
ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: Kwanak-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 256; DB 2; Length 32
Pred. No. 3.9e-76;
0; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,560A
FILLING DATE: 13-NOV-1996
                                                                                                                                                                                                                                                                   Sequence 13, Application US/08737560A Patent No. 5928893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: KR 95-8176 FILING DATE: 08-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY: Republic of Korea
151-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: Republic of Korea
135-110
                                                                                                                                  301 GGGACCAAGCTGGAAATTAA 320
                                                                                                                                                         13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.8%;
Best Local Similarity 87.5%;
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 324 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-NOV-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-737-560A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seoul
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US-08-737-560A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
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                                                                                                                                                                                                                                                                       143 CTTTCCTGCAGGCCAGCCAAAGTATTAGCAACAACCTACACTGGTATCAACAAAAATCA 202
                                                                                                                                                                                                                                                                                                                                                  203 CATGAGTCTCCCAAGGCTTCTCATCAAGTATGCTTCCCAGTCCATCTCTGGGATCCCTCC 262
                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTCTGGGATCCCCTCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCAGT 142
                                                                                                                                                                                                                                                                                                                              121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTGGGATCCCCTCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
                                                                                                                                    Gaps
                                                                                                                                                                     1 GATAITGIGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGGGTCAGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATENT NO. 5453363

PAPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF

TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR

ING ATTER GENETIC EXPRESSION IN PROKARYOTES

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,044

FILING DATE: 02-MAR.1994

PRIOR APPLICATION NUMBER: 942,370

FILING DATE: 09-SEP-1992

PRIOR APPLICATION NUMBER: 498,500

FILING DATE: 23-MAR.1990

FILING DATE: 23-MAR.1990
                                                                                              Length 424;
                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                            Score 296; DB 1;
Pred. No. 2.1e-89;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8.7e-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.2%; Score 289.6; 94.1%; Pred. No. 8.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 GGGACCAAGCTGGAGCTGAA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GGGACCAAGCTGGAAATTAA 320
                                                                                          1 92.2%;
Similarity 95.3%;
05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 76,207
FILING DATE: 23-OCT-1986
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                  23..403
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                                                                                            Query Match
Best Local Simi
Matches 305;
NAME/KEY:
                    ; LOCATION:
US-08-436-463-3
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Matches 301;
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MOLECULE TYPE:
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CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAAAAAATCA
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APPLICANT: KANG, Chang-Yuil
APPLICANT: KING, Chang-Yuil
APPLICANT: KIN, Joéng-Gen
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Republic of Korea
21P: 151-057
ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: Kwanak-gu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,560A
FILING DATE: 13-NOV-1996
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-8176
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08737560A
Patent No. 5928893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Seoul COUNTRY: Republic of Korea ZIP: 135-110 mobu.
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                               GGGACCAAGCTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                            301 GGCACCAAGCTGGAAATCAA 320
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Seoul
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                                              70 to 102 bp hypervariable region CDR1
148 to 168 bp hypervariable region CDR2
265 to 291 bp hypervariable region CDR3
325 to 363 bp 484-1-1 light chain constant region
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APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Immunoglobulin isotype
                                                                                                                                                                                                         Length 363;
                                                                                                                                                                                                                                                      Indels
    bp 4B4-1-1 light chain
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PPLICATION NUMBER: US/08/476,176B
FILING DATE:
                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 5958708artis Patent Department STREEF: 59 Route 10 CTTY: East Hanover STATE: New Jersey
                                                                                                                                                                                                       79.8%; Score 256; DB 2;
87.5%; Pred. No. 4.1e-76;
11ve 0; Mismatches 40
                         variable region
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APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCACCAAGCTGGAAATCAA 320
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CTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-737-560R-8
                                                                                                                                                                                                                                 Best Local Similarity
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Best Local Similarity 82.5
Matches 264; Conservative
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COTHER INFORMATION:
COTHER INFORMATION:
COS-127-721A-3
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US-08-485-246A-3
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                                                                                                                                                                                                                                                                                                                                                                                                      71.8%; Score 230.4; DB 2; Length 322;
82.5%; Pred. No. 1.3e-67;
Live 0; Mismatches 56; Indels 0
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Patent No. 6066718
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kollinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               /product= "light chain variable domain of murine antibody TES-C21"
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                                                        4-19276/A/P2/CIP
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NAME: NO. 5920.
REGISTRATION NUMBER: 35,2.
REFERENCE/DOCKET NUMBER: 4-192
RELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-510
TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                 No. 5958708ak, Henry P. RATION NUMBER: 33,200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 82.59
Matches 264; Conservative
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-476-176B-3
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US-08-127-721A-3
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241 GAAGATATTGCAGATTATTACTGTCAACAAAGTGATAGCTGGCCAACCACGTTCGGAGGG 300
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Patent No. 6072035
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
CORRESPONDENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 322;
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82.5%; Pred. No. 1.3e-67;
iive 0; Mismatches 56;
                   FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR PAPLICATION: 424
PRIOR APPLICATION: 0.7452,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TELEPHONE: 737 has a hairs
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 322 base pairs
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NAKATANI, TOMOYUKI

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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-326-362-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GAIGGITCICCAAGGCITCICAIAAAGIAIGCIICIGAGICIAICICIGIGAACCIICC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GAAGATTTTGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GAAGATATTGCAGATTATTACTGTCAACAAGTGATAGCTGGCCAACCACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.8%; Score 230.4; DB 3; Length 322; 82.5%; Pred. No. 1.3e-67; ive 0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "light chain variable domain of murine antibody TES-C21"
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
                                                                                                                                                                                        PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTOMNEY/AGENT INFORMATION:
NAME: NO. 6072035ak, Henry P.
REGISCHEATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
TELEPHONE: CHARACTENISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/08232081B Patent No. 5886152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GGGACCAAGCTGGAGATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGGACCAAGCTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.8
Best Local Similarity 82.5
Matches 264; Conservative
                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION: 1..321
CTHER INFORMATION:
CTHER INFORMATION:
US-08-485-246A-3
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                07936-1080
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               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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121 CATGAGICICCAAGGCTICICAICAAGIATCGTICCCAGICCAICTCTGGGAICCCCTCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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81.2%; Pred. No. 1.7e-65;
live 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/??
                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SYENSON, LEDNARD R
REGISTRATION NUMBER: 30,330
REFRENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          STATE: VA
COUNTY: USA
ZOUGHTY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GGGACCAAGCTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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US-08-232-081B-39
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301 GGGACCAAGCTGGAGAT 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                        APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATGGTTCTCCAAGGCTTCTCATTAAGTATTCTTCTGAGTCTATCTTGGGATCCCTTCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGACACCAGGAGATAGCGTCAGT
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                                                                                                                                                                                             Garrett
                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 219.4; DB 1;
Pred. No. 5.9e-64;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Einaudi, Carol P.
RECISTRATION NUMBER: 32,220
REFERENCE, POCKET NUMBER: 02481-1276-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabov
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE P 42 08 795.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION APR:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION UNUMBER: DE P 42 08 795.:
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         STAIL.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
Sequence 3, Application US/08326362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
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80.8%;
                                                      Bosslet, Klaus
Seeman, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.8°
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                    GENERAL INFORMATION:
APPLICANT: Bossle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
US-08-326-362-3
                                                                                                                                                                                                                                                                       0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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121 AATGGTTCTCCAAGGCTTCTCATAAAGTATGCTTCTGAGTCTATCTCTGGGATCCCTTCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAGTCCATCTTTGGGATCCCTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTGTGACACCAGGAGATAGCGTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 318;
                                 APPLICANT: WELS, WINFRIED S.
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATHIAS
APPLICANT: VAKALOPOULGU, EVANGELIA
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILITEN ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELB PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/AKS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13*FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
                                                                                                                                                                                                                                                                                                SSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. 2200 CLARENDON BLVD. SUITE 1400 ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.2%; Score 218.8; DB 2; Best Local Similarity 80.5%; Pred. No. 9.4e-64; Matches 256; Conservative 0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: SCH 1576
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other nucleic acid
US-08-800-198-3
Sequence 3, Application US/08800198
Sequent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Search completed: October 11, 2001, 15:14:15 Job time: $5002\ \text{sec}$

em_pl:*
em_ro:*
em_sxs:*
em_sy:*
em_yr:*
em_vi:*
em_vi:*
gb_sts1:*
gb_sts3:*

gb_un:* gb_vil:* gb_vi2:*

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                 October 11, 2001, 15:09:32 ; Search time 2122.65 Seconds (without alignments) 2339.127 Million cell updates/sec
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321
1 GAGATTGTGCTAACTCAGTC.......GGACCAAGGTGGAAATTAAG 321
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Database :

AX060782 Sequence AX060786 Sequence AX060786 Sequence M35943 Mouse IRNA M35667 Mouse Iysoz M93959 Mouse Ig ac AR163757 Mouse Ig ac M95945 Mouse mRNA

MUSIGKACY MUSIGKACY MUSIGKXD AF163757 MUSCMVH

AX060782 AX060810 AX060786

Description

SUMMARIES

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Anti-_g(a) v?_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use Patent: WO 0078815.4 31 28-DEC-2000; Applied Molecular Evolution (US)
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Pred. No. 5.2e-86;
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                               Score 318.6; DB 9
Pred. No. 3.4e-86;
2; Mismatches 1
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Sequence 31 from Patent WO0078815.
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Huse, W.D. and Wu, H.
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X02234 Mouse mRNA
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RLIKYRSQSISGIFARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGT
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1 (bases 1 to 321)
Huse,W.D. and Wu,H.
Anti-g(a) v?_g(b)37 recombinant human antibodies, nucleic acids encoding same and methods of use Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
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/db_xref="taxon:32630"
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AF139846
AF045514
MMU40581
AF113242
AF113243
MMU277215
MMU277215
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MMX16070
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 321) Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S., Co.M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L. Untitled
                                                                                                                                       Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA
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imunoglobulin light chain; immunoglobulin-kappa; processed gene;
variable region VK23.
Mouse hybridoma, cDNA to mRNA, clone 10K-106.
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Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
mRNA, partial cds.
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/organism="Mus musculus"
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Best Local Similarity 85.3%;
Matches 273; Conservative
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Above="01:12406167"
/translation="DIVIDGSPATLSYPPGDSVSLSCQASQSISNHLHWYQQKSHESP
RLIKYRSQSISGIPSRFSGSGSGTDFALSINSVETEDFGMYFCQQSGSWPHTFGGGT
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1 (bases 1 to 321)
1 (bases 1 to 321)
1 (bases 1 to 321)
2 and Mu.H.
Anti-g(a) v?_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use Patent: Wo 0070815-A 7 28-DEC-2000; Applied Molecular Evolution (US)
Location/Qualifiers
                                               GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT 240
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Pred. No. 3.9e-70;
2; Mismatches 34
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                         AX060786 321 bp DNA
Sequence 7 from Patent WO0078815.
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                                                                                                                                      /codon_start=1
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Best Local Similarity 88.8%;
Matches 285; Conservative
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SNSWRPHFGSGTKLEFRRADA"

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Mus musculus mAb 101.4.1 immunoglobulin light chain variable region
mRNA, partial cds.
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Metrens, M.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
Mouse Monoclonal Antibodies
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Mertens, N. M. and Cunningham, M.W.
Direct Submission
Submitted (03-7UN-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCTCAGTATCAACAGTGTGGAGACT 276
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Pred. No. 1.8e-64;
2; Mismatches 45; Indels
                                /organism="Mus musculu
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                                                                                                                                                                                                                                                     /gene="IgK"
/note="putative"
                                                                                                                                                                                                                                                                                                                          /codon_start=1
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85.3%;
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/gene="IgK"
1. .370
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Matches 273; Conservative
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/note="lysozyme binding Ig kappa chain V23-J2 region"
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Nucleotide sequences of immunoglobulin heavy and light chain
V-regions from a monoclonal autoantibody specific for a unique set
of small nuclear ribonucleoprotein complexes

Nucleic Acids Res. 20, 4099-4099 (1992)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 370)
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                                                          1 (bases 1 to 321)
Mainhart,S.-G.-S.J., Lavoie,C., Feldman,T.B., Drohan,R.J. and
Brooks,W.B.R.
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Pred. No. 1.8e-64;
2; Mismatches 45; Indels 0;
                                                                                                                                                      A three-dimensional model of an anti-lysozyme antibody
J. Wol. Biol. 194, 713-724 (1987)
88011212
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Mouse Ig active kappa-chain V-region, partial cds.
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/organ1sm="Mus musculus"
/db_xref="taxon:10090"
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Mus musculus CDNA to mRNA.
Mus musculus
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85.3%;
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181

DEFINITION ACCESSION VERSION KEYWORDS

MUSIGKXD

ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE FEATURES

216 240

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Query Match

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BASE COUNT

ORIGIN

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FEATURES

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240 240

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E07933 381 bp RNA PAT 29-SEP-1997 Channel and anti-FHV-1 antibody L chain. E07933.1 GI:2176065
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1. .381
/product='variable region of mouse anti-FHV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKATYOTA; METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Masses 1 to 31, Roses 1
                                                                                                                                                                                                                                                                                                               61 CTTTCCTGCCAGGCCAGCCAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp. (mouse)
JP 194217786-A/2
09-AUG-1994
28-NOV-1992 JP 1992341255
KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAWA KIYOTO, PI
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                                                                                                                         DB 94; Length 321;
                                                                                                                                                                      Indels
                                                                                                                       Score 245.6; DB 94;
Pred. No. 5.5e-64;
2; Mismatches 46;
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1. .381
/organism="Mus sp."
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topology: Linear;
hypothetical: No;
/note="putative"
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Best Local Similarity 85.0%;
Matches 272; Conservative
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PF 28-NOV-1992
PI XURUNI
TOKIXOSHI YUKIO
PC C12P21/08.A6
CC strandedness
CC topology: Li
CC hypothetical
CC anti-sense:
FH cource
FT source
FT mat_peptide
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/product="immunoglobulin light chain variable region"
/protein_id="AAD47036.1"
/db_xref="GI:5690321"
/translation="DIVLTQSPATLSVTPGDSVSLSCRASQSISNNLHWYQQKSHESP
RILIKYASQSISGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQSNSWPLTFGAGT
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Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S., Co.M.S., Vasguez,M., Britt,W.J. and Coelingh,K.L. Untitled Unpublished (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA Mus musculus
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/db_xref="taxon:10090"
/cell_line="MAb 5"
/cell_type="hybridoma"
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/organism="Mus musculus"
                                                 1. .321
/organism="Mus musculus"
                                                                                            /strain="BALB/c"
/db_xref="taxon:10090"
/note="mAb 101.4.1"
                      ocation/Qualifiers
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1 (bases 1 to 381)
Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelingh,K.L.
  241 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
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                                                                                                                                                                                                                                Unclassified.

1 (bases 1 to 381)

Queen, C.L., Schneider, W.P. and Selick, H.E.
Polynuclectides encoding improved humanized immunoglobulins
Patent: US 569761-A 82 02-DEC-1997;
                      1 GAGATTGTGCTAACTCAGCCACCACCAGTCTCTCAGCCCAGGAGAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTCCTGCCAGGCCAAGCAATATTAGCAACCACCTACACTGGTATCAACAAAGGCCT
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Pred. No. 5.4e-64;
2; Mismatches 46;
                                                                                                                                            178571 381 bp DNA
Sequence 82 from patent US 5693761.
178571
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US
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Best Local Similarity 85.0%;
Matches 272; Conservative
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Pred. No. 5.4e-64;
2; Mismatches 46
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Queen,C.L. and Sellck,H.E.
Humanized immunoglobulins
Patent: US 5585089-A 82 17-DEC-1996;
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/db_xref="taxon:10095"
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131959
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Draft entry and computer-readable sequence [2] kindly submitted by
G.Rule, 20-JUL-1988.
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Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 56)
                                                                                                                                                                                                                           CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACAGGTATCAACAAAAGGCCT 120
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Unpublished (1988)
Upublished (1988)
Upublished (1988)
Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
bodies for NMR studies
Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
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C-region; immunoglobulin light chain; immunoglobulin-kappa;
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/strain="BALB/c"
/sub_species="domesticus"
/db_razon:10090"
/cell_type="mature B cell"
33. 92
              Humanized immunoglobulins
Patent: US 5693762-A 82 02-DEC-1997;
Location/Qualifiers
1, .381
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                                                                    /organism="unknown"
92 c 89 g
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/codon_start=1
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/product="immunoglobulin kappa-chain"
/product="immunoglobulin kappa-chain"
/db_xref="d1:197034"
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ASSYSONLHWFOQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVETED
FGMYFCQQSNSWPFTFGGGTKLEIKRADAAP"
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Brard, F., Shannon, M., Prak, B.L., Litwin, S. and Weigert, M. Somatic mutation and light chain rearrangement generate autoimmunity in anti-single-stranded DNA transgenic MRL/1pr mice 9406777
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Brard,F. and Weigert,M.
Brisch Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University, Washington Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
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Mus musculus clone 50 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
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/cell_type="B cell hybridoma (spontaneous fusion with
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/db_xref="taxon:10090"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                           Score 245.6; DB 94; Length
Pred. No. 5.4e-64;
2; Mismatches 46; Indels
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107 c 102 g 109 t
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Best Local Similarity 85.0%;
Matches 272; Conservative
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/codon_start=1
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Vk23"
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Brard, F., Shannon, M., Prak, E.L., Litwin, S. and Weigert, M. Sometic mutation and light chain rearrangement generate autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice 9406777
                                                                                                                                       Direct Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              /cell_type="B cell hybridoma (spontaneous fusion with SP2/0)"
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/gene="IgG"
/note="CDR1; complementarity determining region 1"
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                                                                                                                                                                                                                                                     /strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/chromosome="6"
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Pred. No. 1.7e-63;
2; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="IgG"
/note="variable region (VJ)"
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                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="spleen"
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                                                                                                          2 (bases 1 to 324)
Brard, F. and Weigert, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265. 291
/gene="IgG"
/note="CDR3; c
287. 30
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/gene="IgG"
/note="CDR2;
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/note="Jk2'"
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nilarity 84.7%;
Conservative
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Best Local Similarity
Matches 271; Conserv
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/translation="DIVLTQSPATLSVTPGESVSLSCRASQSISNNLHWFQQKSHESP
RLLIKYASLSISGIPSRFIGSGSGTDFTLSINSVETEDFGMYFCQQSDNWPHTFGSGT
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                                                                                                                                               'product="immunoglobulin kappa light chain variable region
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Memmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
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Mus musculus clone 38 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
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Pred. No. 1.3e-63;
1; Mismatches 47; Indels 0;
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/gene="lgG"
/note="CDR1; complementarity determining
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/gene="19G"
/note="CDR2; complementarity determining
265. .291
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                                                      /gene="IgG"
/note="variable region (VJ)"
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                                                                                                                                                                                  /protein_id="AAD28631.1"
                    /tissue_type="spleen"
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/gene="IgG"
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Best Local Similarity 85.0%;
Matches 272; Conservative
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/gene="IgG"
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	99_est63:* 90_est64:* 90_est66:* 90_est75:* 90_est775:* 90_est776:* 90_est776:* 90_est776:* 90_est78:* 90_est81:* 90_est81:* 90_est81:* 90_est81:* 90_est81:* 90_est81:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est86:* 90_est80:* 90_est80:* 90_est80:*		esth esth esth esth estr estr estr estr
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Location...

1. 738...

1. 738...

/organism="Mus musculus"
/strain="FVB/N"
/db_xere="axon:10090"
/clone="ImMGE:41]4012"
/clone="ImMGE:41]4012"
/clone="Imbac="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 949)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CTGCCAGGCCAAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAGGCCTGGTCA 125
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                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
f column: 11
High quality sequence stop: 714.
Location/Qualifiers
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCCAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.7%; Score 217.2; DB 150; Length 738; Best Local Similarity 84.0%; Pred. No. 3.3e-56; Matches 267; Conservative 2; Mismatches 45; Indels 4;
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BF579007
BF579007.1 GI:11652719
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FEATURES

BASE COUNT ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherlia; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 434)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CITICCIGCCAGGCCAGCCAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
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                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1566 row: e column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 206; DB 155; Length 946;
Pred. No. 1e-52;
1; Mismatches 71; Indels 0
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                                                                                                                                                                                 High quality sequence stop: 738.
Location/Qualifiers
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al Similarity 77.5%;
248; Conservative
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Matches 248;
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/clone_lib="NCI_CGAP_CO24"
/clone_lib="NCI_CGAP_CO24"
/lab_host="Dilib" Colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov.p column: 05

High quality sequence start: 9

High quality sequence stop: 730.

Location/Qualifiers

1. 949

// Arganism="Mus musculus"

// Arganism="Mus musculus"

// Alb Arganism="Mus musculus"

// Alb Arganism="Mus musculus"

// Alb Arganism="Mus musculus"

// Alb Arganism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 GTCTCCGAGGCTTCTCATCAAGTTTGTTTCCCAGTCCATCTCTGGGATCCCTCCAGGTT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 949;
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Pred. No. 1.9e-54;
2; Mismatches 56; Indels
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Best Local Similarity 81.2%;
Matches 255; Conservative 5
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ACCESSION VERSION KEYWORDS

RESULT BG569760

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AUTHORS TITLE JOURNAL

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                                                                 AUTHORS
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                       National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contect: Robert Strausberg, Ph.D.
Email: cgapbs riemail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CNA Library Arrayed by: M.B. Soares Lab
COMP Attribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: MI3 Forward.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 AGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGGGG
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Pred. No. 1e-52;
1; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens'
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                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity 77.7%;
Matches 247; Conservative
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                             TITLE
JOURNAL
COMMENT
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Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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1 (bases 1 to 398)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                    Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Exo RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clond Library Arrayed by: M.B. Soares Lab

Clond distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Pred. No. 2.4e-52;
1; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3059305"
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1. .398
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Best Local Similarity 77.2%;
Matches 247; Conservative
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/lab_host="Delta" | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Moderate | Mo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGATIGIGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
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                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Econ II stapes-remain.inflow
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution informa found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
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Pred. No. 2.5e-51;
1; Mismatches 74; Indels
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1. .519
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AW405025.1 GI:6924082
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Best Local Similarity 76.6%;
Matches 245; Conservative
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                                         l (Dases I to 482)

Yangy Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu
,W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J.,
Chen, Z. and Han, Z.
Homo sapiens cDNA cdA clones
Unpublished (2000)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 519)
NIH-MGC http://mgc.ncl.nih.gov/.
                                                                                                                                                                                                                       Contact: Zeguang Han
Contact: Zeguang Han
Contact Mational Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922.
Emali: hanzgédnc:sh.cn
This clone is available at CHGC in Shanghai.
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t 1 others
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UI-HF-BLO-acb-b-10-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058506 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 CTCTCCTGCAGGCCCAGTCAGAAGCAGCTCCTTAGCCTGGTACCAACAGAAACCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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152 c 122 g 111
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76.98;
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DB 115; Length 519;

9 Gaps

240

REFERENCE AUTHORS TITLE JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 46 primates) 1 to 46 primates; I to 46 primates; Marional Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                           Unpublished (1999)
Ontact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Enoil: cgapbs-rémail.nih.gov
Enoil: cgapbs-rémail.nih.gov
Enoil: site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.AGE. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 199.6; DB 1 Pred. No. 7.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .468
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057561"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGACCAAAGTGGATATCAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:9160297
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Best Local Similarity 76.2
Matches 244; Conservative
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BE306691
BE306691.1 GI:
EST.
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JOURNAL
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KEYWORDS
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                                                                                                                                          AUTHORS
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1. 385

(organism="Homo sapiens"

(bb xref="taxon:9606"

(clone="IMAGE:3058252"

(clone="IMAGE:3058252"

(clone="IMAGE:30Faming Coll_type="germinal center B cells"

(cell_type="germinal center B cells"

(cell_line="MGC85"

(redl_type="germinal center B cells"

(cell_line="MGC85"

(cell_line="MGC85"

(lab_host="Hom108" (LTI)"

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

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(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

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(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

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(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;

(note="Vector: pT773-Pac; Site_1: NotI; Site_1: NotI; Site_1: PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT773-PT7
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                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov

BCo RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbry/image/image.html

Seq primer: MI3 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 TCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCCAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGA 246
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                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW405643 468 bp mRNA EST 16-FEB-2000 UI-HF-BL0-abs-f-05-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057561 5', mRNA sequence.
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Pred. No. 3e-51;
1; Mismatches 73; Indels
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AW405643.1 GI:6924700
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Best Local Similarity 76.7%;
Matches 244; Conservative
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               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gibbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C2ECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3501355"
/clone="IMAGE:3501355"
/closue=Lype="spontaneous tumor, metastatic to mammary.
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                             61 CTTTCCTGCCAGGCCAAGGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW404506 468 bp mRNA EST 16-FEB-2000
UI-HF-BLO-aby-a-05-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058065 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AGGITCAGIGGCAGIGGAICAGGGACAGAITICACCCICACIAICICCAGICIGGAGCCI
                                                                                                                                                                                                                                                                                                                                                          Query Match 62.1%; Score 199.2; DB 166; Length 624; Best Local Similarity 75.9%; Pred. No. 1.1e-50; Matches 243; Conservative 2; Mismatches 75; Indels, 0;
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359 GGGACCAAGCTGGAAATAAA 378
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AW404506.1 GI:6923563
house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                           172
       ORGANISM
                                  REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                        COMMENT
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/clone="luAge:3058065"
/clone=lib="NHH_MGC_37"
/tissue_type="Lymph"
/cell_type="germinal center B cells"
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/lab_host="DH10B (LTI)"
/note="Vector: pr773-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pr773-Pac; Site_1: NotI; Site_2: Eco RI;
(1.5-2.5kb). Directionally cloned cells provided by Louis
Bonaldo, Ph.D. Library preparation by Maria de Fatima
80 a 137 c 114 g 111 t Soares, Ph.D."
ENARTORIA METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 468)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CNA Library Preparation: M.B. Soares Lab

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Seq Primer: M13 Forward.
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Pred. No. 2.4e-50;
1; Mismatches 76; Indels 0
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Best Local Similarity 75.9%;
Matches 243; Conservative 1
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Sfil (ggcgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATPATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGAGCGGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library.

284 c 251 g 205 t 2 others
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                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The J.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1509 row: k column: 22
http://image.llnl.gov
Plate: LLCM1509 row: k column: 22
high quality sequence stop: 624.
Location/Qualifiers
rce // Organism="Homo sapiens"
// Ab_xref="taxon:9606"
// Clone="ImAGE:461089"
// Ab_host="DH10B" (Tl phage-resistant)"
                                                                                     Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 3e-50;
1; Mismatches 76;
                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                     Chordata;
Primates;
 BG536848
BG536848.1 GI:13528394
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75.98;
                                                                                     Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 1015)
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Matches 243; Conservative
                                                                      Homo sapiens
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/clone="INAGE:305806"
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

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National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Preparation: M.B. Soares Lab

CNA Library Prayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llni.gov/Dbrp/Aimage/image.html
Seq primer: MJ3 Forward.
                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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AW404697 465 bp mRNA EST 16-FEB-2000 UI-HF-BLO-acd-b-04-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058518 5', mRNA sequence.
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Pred. No. 7.4e-50;
1; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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1. .465
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AW404697.1 GI:6923754
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Best Local Similarity 75.6%;
Matches 242; Conservative
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GGGACCAAGGTGGAAATTA 319
                                                Query Match
Best Local Similarity 75.3:
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                               human.
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ISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhin1; Hominidae; Homo.

I (bases 1 to 548)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be http://image.llnl.gov.

Plate: LLCM1564 row: m column: 13

High quality sequence stop: 548.

Location/Qualifiers

I A.B. Sequence stop: 548.
                                             BG568486 548 bp mRNA EST 10-APR-2001 602587455F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716468 5',
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Pred. No. 1.6e-49;
1; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4716468"
                                                                                                                                         BG568486.1 GI:13576139
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Matches 241; Conservative
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Endammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RS Yang,Y., Song,H., Peng,Y., Gu,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Vi, Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
M., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
M., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
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M., Tu,Y., Song,Han, Chan,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
M., Tu,Y., Song,Han, Canda clones

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AV734882 A85 bp mRNA EST 17-OCT-2000
AV734882 cdA Homo sapiens cDNA clone cdABFC04 5', mRNA sequence.
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/dev_stage="Adult"
/lab_host="BM25.8"
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Pred. No. 2.3e-49;
1; Mismatches 78
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/organism="Homo sapiens"
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                                                                                                  AV734882.1 GI:10852427
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cDNA encoding kapp Humanised antibody

Humanised antibody EGF receptor chime

Murine vitronectin Mouse anti-verotox Human secreted exp hIL2R Ab L chain V Expression vector Light chain coding Mouse monoclonal a Jk gene segment. Humanised anti-alp

L-chain V-region o

Perfect score:

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Anti-gp54 MAD 48-1
Plasmid pWW152-225
Plasmid pSW202-225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LM609 antibody light chain variable region DNA grafted fragment.
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                                                                                                                                          AAQ43245
AAZ10202
AAT38510
AAD01262
AAV71803
AAV71805
AAZ10203
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AAZ10205
AAF29505
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AAN90300
AAQ43243
AAV26766
AAQ43384
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AAV26770
                                                     AAA44346
AAT49345
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AAD00906
AAT33446
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AAA40203
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   AAV49843 standard; DNA; 321
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Copyright (c) 1993 - 2000
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    nucleic search, using sw model

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                                                                                                                                                  This sequence encodes a LM609 grafted antibody variable light chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 and can be used to inhibit binding of alphavbeta4 of a ligand and thus block integrin-mediated signal transduction. This is useful in specifically angiogenesis and restenosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psorlasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
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ilarity 100.0%; Pred. No. 2.9e-91.
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Pred. No. 6.9e-91;
2; Mismatches 1;
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                                                 Location/Qualifiers
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99.1%;
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Matches 318; Conservative
                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huse WD;
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Unidentified

LM609;

28-DEC-2000

03-APR-2001

AAF28176;

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AAF28176 RESULT

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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of anglogenesis, inflammatory diseases e.g. psoriasis, cancers and
61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctttcctgccaggccaggccaagtattagcaaccacctacactggtatcaacaaaggcct 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                            LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                       DNA encoding light chain variable region of LM609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 318; DB 22;
Pred. No. 1.1e-90;
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                                                                                                                                                                                                   BP.
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99.1%;
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                                                          GGGACCAAGGTGGAAATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTCCTGCCAGGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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Pred. No. 6.9e-91;
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                                                                                                                                                                            Vitaxin light chain variable region DNA.
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                                                        BP.
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99.1%;
                                                          DNA; 321
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                                                        AAF28176 standard;
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Length 321; Indels us-08-791-391a-31.rng

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Sequence 321 BP; 83 A; 83 C; 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the LM609 antibody variable light chain region.

LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
and can be used to inhibit binding of alphavbeta3 to a ligand and thus
block integrin-mediated signal transduction. This is useful in the
treatment, prevention and diagnosis of alphavbeta3-mediated disease,
specifically angiogenesis and restenosis (but also e.g. (non-)immune
inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
etc.). The antibodies contain non-murine framework regions so are
suitable for use in humans. Enhanced types of LM609 have affinity more
than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "LM609 antibody light chain variable region"
/note= "partial sequence, no start or stop codon given"
                                                                          181 aggttcagtggcagtggatcagggacagatttcaccctcactatctccagtctggagcct 240
                                                                                                               300
   121 ggtcaagccccaaggetteteatennntategtteecagteeatetetgggateecegee 180
                                                                                                                                                 241 gaagattttgcagtctattactgtcaacagagtggcagctggcctcacacgttcggaggg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                               GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                        AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                  LM609 antibody light chain variable region DNA fragment.
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                                                                                                                                                                                                                          301 gggaccaaggtggaaattaag 321
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                                                                                                                                                                                                                       Enhanced LM609 grafted antibodies exhibiting selective binding affinit to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
                                                                                                                                                                                                                                                                                       GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                              CTTTCCFGCCAGGCCAAAGTAFTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                 Gaps
                                                                                                                         1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
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                                                                                                                                                                                                                                                                                                                                                                                  AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
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Length 321;
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                                              Indels
  DB 19;
                                                 34;
Score 265.8; DB 1
Pred. No. 2.9e-74;
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                                              2; Mismatches
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82.8%;
88.8%;
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                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteoporosis
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                                              Matches 285;
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                                                                                                                                                             CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                        241 gaagattttggaatgtatttctgtcaacagagtggcagctggcctcacacgttcggaggg 300
                                                                                                          Gaps
                                                                                                                          1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAGGGCGACT 60
                                                                                                                                    monoclonal antibody; light chain; mouse; human; humanised antibody; Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
          of
                                                                                                                                                                       GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTTGGGATCCCCGCC
                                                                                                                                                                                                                                                                       GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                                                                                                                                   181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                disorders associated with inappropriate or inopportune invasion vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                         ;
0
                                                                                       Length 321;
chronic articular rheumatism),
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised anti-verotoxin II antibody VTm1-1 VL cDNA.
                                                                                       DB 22;
                                                                                                          34;
                                                             Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
                                                                                       Score 265.8; DB 2:
Pred. No. 2.9e-74;
                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
diseases (such as psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TEIJ ) TEIJIN LTD.
(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                       AAZ35244 standard; cDNA; 381 BP
                                                                                                                                                                                                                                                                                                                    301 gggaccaagctggaaattaag 321
                                                                                                                                                                                                                                                                                                          301 GGGACCAAGGTGGAAATTAAG 321
                                                                                      Query Match 82.8%;
Best Local Similarity 88.8%;
Matches 285; Conservative
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/*tag=
61..381
/*tag=
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                                             osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
Synthetic.
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This DNA sequence codes for a humanised light chain variable region (see AAY32407) of murine monoclonal antibody VTml-1 (MuVTml-1), an antibody that specifically binds to the B subunit of verotoxin II (VT2). The invention relates to humanised autibodies against VT2 that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVTml-1 comprissing the complementarity determining regions of MuVTml-1 (see AAY32404-05) and heavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain variable region frameworks from the human GF4 antibody heavy are used from Ld9, H29, H30, H39 and H38 is occupied by the mino acid at the equivalent position of the MuVTml-1 antibody heavy or light chain variable region framework. Such humanized antibodies have an affinity for VT2 that is 3., 5 or 10 times that of MuVTml-1. The toxic effects from VT2 (laimed), especially for treating a patient suffering from, or at risk of, verotoxin producing Escherichia coil (VTBC) infection, and haemolytic
                                                                                                                                                            for treating Verotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 gaagattttgcagtgtattactgtcaacagagttacagctggccgctcacgttcggtcaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
   Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGATIGIGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 gaaattgtgctaactcagtctccagccaccctgtctgtgtctccaggagaaagagccact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ggtcaggctccaaggcttctcatcaagtctgcttcccagtccatctctgggatccccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCCT
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Vasques
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mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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2; Mismatches 38; Indels
CO MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VL cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;
                                                                                                                                                            nsed
Takedo T,
                                                                                                                                                            binding to verotoxin II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.5%; Score 258.4;
87.5%; Pred. No. 6.56
Kimura T,
                                                                                                                                                                                                                                                  Disclosure; Fig 2b; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV71800 standard; cDNA; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Imaizumi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 87.5
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uraemic syndrome (HUS).
                                                           2000-086580/07.
                                                                                                                                                     Humanized antibody producing E. coli -
                                                                                             P-PSDB; AAY32407
Matsumoto Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1999
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cancer; metastasis; rheumatoid arthritis; atherosclerosis;

Thu Oct 11 16:16:17 2001

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This born sequence couche in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gacatagtactgactcagtctccaggcaccctgtctttgtctccaggagaaagagccacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New anti alpha_v beta_3 vitronectin receptor antibodies - used immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      They can also be used for targeted drug
                    anglogenesis; diabetic retinopathy; inflammation;
macular degeneration; osteoporosis; Paget's disease;
hyperparathyroldism; hypercalcaemia; therapy; immunotherapy;
D12RRMC-10; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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85.9%; Pred. No. 2e-6
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy, and for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 61-62; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                            97US-0039609.
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Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jonak ZL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-034590/03.
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                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johanson KO,
                                                                                                                                                                                                                         WO9840488-A1
                                                                                                                                                                                                                                                                                                                             12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis
                                                                                                                                                                                                                                                                           17-SEP-1998
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expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; MAb; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This DNA sequence codes for the region of the murine monoclonal antibody (MAb) D12 light chain variable region (VL, see AAW85000) that is altered in humanised D12 VL (see also AAW8408B), including the first 5 amino acids of the human kappa constant region. It was prepared from 4 overlapping synthetic oil gonucleotides (see AAV71816-19). The synthetic gene was used to construct an expressi vector for humanised D12 VL. D12 is an anti-alpha-v beta-3 vitronectin receptor MAb. Humanised D12 MAbs can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New anti alpha_v beta_3 vitronectin receptor antibodies - used for immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
aggttcagtggcagtggatcagggacagatttcactctcaccatcagccgtctagagcct
                             GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                              mouse, human; vitronectin, alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 250.4; DB 20; Length 338;
Pred. No. 2.1e-69;
Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 338 BP; 82 A; 99 C; 79 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                    Vitronectin alpha-v beta-3 MAb VL cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Page 64; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                         AAV71802 standard; cDNA; 338
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85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US04987.
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                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-034590/03.
P-PSDB; AAW84100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johanson KO,
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Best Local Simil
Matches 275; C
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                                                                                                                                                                                                                                                                     15-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Synthetic.
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Length 381; Indels

DB 15; 46; 180 240 240 300

Phase Park

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Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACAGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                              GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                      1 GAGATIGIGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                     121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                                                       and fragments of VH and VL CDR1, CDR2 and CDR3. The antbodies are used in the detection, treatment and prevention of FHV-1. The sequences of the CDRs in the VH of the recombinant anti-FHV-1 antibody are given in AARS4092. The sequences of the CDRs in the the recombinant anti-FHV-1 antibody are given in AARS4093. These
                                                                                                                                                                                                                                                                                                                                                                               AGGTTCAGTGGCAGTGGATCAGGACAGATTTCACCTTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.
                                                                                                    Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;
                                                                                                                                             Score 245.6; DE
Pred. No. 7e-68;
                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gggaccaagctggagctgaa 380
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                                                                                                                                             76.5%;
85.0%;
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89US-0310252
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                                                                                                                                                                            Conservative
                                                                           sequences are claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selick HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-190856/19.
                                                                                                                                                            Similarity
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13-FEB-1989;
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19-DEC-1990;
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                                                                                                                                                                         272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF58747;
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Best Local
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Matches
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                                                          GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                   GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The inventors claim a monoclonal antibody against feline herpes virus (FHV-1). They also claim a recombinant antibody against FHV-1
AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of mouse V-kappa showing the sequences of recombinant anti-FHV-1 antibody CDRs 1, 2 and 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feline monoclonal antibody and recombinant antibodies specififor FHV-1 - for detection, treatment and prevention of FHV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feline herpes virus; FHV-1; monoclonal antibody; CDR; complementarity determining region; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tokiyoshi
                                                                                                                                                                                                                                                                                                                                                                           AAQ64167 standard; cDNA to mRNA; 381 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 18-19; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/label= MKL104
385..429
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/label= MJK124
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                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-200288/24.
P-PSDB; AAR54093.
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AAQ64167

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                                                                                The present invention describes a method of producing humanised humanoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is sobtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections and myeloid leukaemia. The present sequence is an antibody cDNA used to
                                                                                                                                                                                                                                                                                     CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                        ctttcctgcagggccaaagtattagcaacaacctacactggtatcaacaaaatca 180
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                                                                                                                                                                                                                                                                          1 GAGATIGIGCTAACTCAGICICCAGCCACCCIGICTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                        GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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                  Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell-
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                   Length 381;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pBT111 encoding antibody MAK33 kappa chain.
                                                                                                                                                                                                   Sequence 381 BP; 97 A; 92 C; 89 G; 103 T; 0 other;
                                                                                                                                                                                                                                  Score 245.6; DB 22;
Pred. No. 7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7..663
/*tag= a
/product= kappa chain of MAK33
                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                              demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody MAK33; kappa chain; plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                             Example 8; Fig 39; 145pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 gggaccaagctggaaataaa 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ04654 standard; DNA; 5238
                                                                                                                                                                                                                                 Query Match 76.5%;
Best Local Similarity 85.0%;
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88DE-3835350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
P-PSDB; AAB69687
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Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding the Fd chain of antibody MAK33 were used to transform E.coli DSW 3689 and the resulting cells grown to form inclusion bodies. After the final renaturation step an 18% yield of biologically active protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catgagtctccaaggcttctcatcaaatatgcttcccagtccatcttgggatcccctct 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised antibody; monoclonal antibody; MAD; antibody engineering mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoprosis; Paget's disease, hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 5238;
                                                                                                                                                                                                                                    Activated antibody prodn. from recombinant procaryotic cells by solubilisation under reducing conditions, then oxidative renaturation, carried out at low protein concn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 239.6; DB 1
Pred. No. 1.4e-65;
1; Mismatches 50
                                                          (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.6%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV71798 standard; cDNA; 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 84.1
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                         Disclosure; ; p; German
                                                                                                                  Buchner J,
                                                                                                                                                                            WPI; 1990-156813/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see also AAQ04655
17-0CT-1988;
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                                                                                                                  Rudolph R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV71798;
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See AAW84004) of the anti-human alpha-v beta-3 vitronectin receptor murine monoclonal antibody D12. It was obtained from hybridoma total RNA by RT-FCK using mouse kappa and N-terminal-based primers (see AAV71808-09). A heavy chain variable region clone (see AAV7197) has also been identified. D12 VH and VL show sequence similarity to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see AAW84096), respectively. Humanised VH (see AAW84096), respectively. Humanised VH (see AAW84098) were constructed by combining the framework regions of the human V region consensus sequences with complementarity determining regions of D12 (keeping some preferred murine framework residues). The humanised antibodies are specifically reactive with the human seceptor. They can be used for passive immunotherapy of a disorder receptor. They can be used for passive immunotherapy of a disorder disorders or angiogenic-related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and a such consensus associated with diabetic retinopathy, atherosclerosis and a such consensus associated with diabetic retinopathy, atherosclerosis and a such consensus associated with diabetic retinopathy, atherosclerosis and a such consensus associated with diabetic retinopathy, atherosclerosis and a such consensus associated with diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restenosis, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis, hyperparathyroidism, Paget's disease, hypercalcemia of malignancy, osteolytic lesions produced by bone metastasis, bone
                                                                                                                                                                                                                                                                                                                                                                                                New anti alpha_v beta_3 vitronectin receptor antibodies - used for immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA sequence codes for the light chain variable region (VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 59-60; 97pp; English.
                                                                                                                                                                                                                                                                     Taylor AH;
                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                        98WO-US04987.
                                                                                                                                                            97us-0039609
                                                                                                                                                                                                                                                                     Jonak ZL,
                                                                                                                                                                                                                                                                                                                   WPI; 1999-034590/03.
                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW84094.
                                                                                                                                                                                                                                                                  Johanson KO,
WO9840488-A1
                                                                                                                                                            12-MAR-1997;
                                                                                                        12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis
                                                    17-SEP-1998
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                                                                                                                61 CITTCCTGCCAGGCCAGCCAAGTATTAGCAACCCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                        121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                         AGGTTCAGTGGCAGTGGATCAGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT 240
                                                                                                                                                                                                                                                 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                           ctttcctgcagggccaggccaaagtattagcaaccacctacactggtatcaacaaagatca 120
                                                         1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAGGGCGACT 60
                                                                         ó
   DB 20; Length 324;
Score 239.2; DB 2
Pred. No. 6.8e-66;
2; Mismatches 50
Query Match 74.5%;
Best Local Similarity 83.8%;
Matches 268; Conservative 2
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Length 381;

DB 21;

Score 232.8;

72.5%;

Query Match

Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;

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This DNA sequence codes for the light chain variable region (see AXY32465) of murine monoclonal antibody VTml-1 (MuVTml-1), an antibody that specifically binds to the B subunit of verotoxin II (VT2). The invention relates to humanised antibodies against VT2 that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVTml-1 comprising the complementarity determining regions of MuVTml-1 and heavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain trameworks. Provided that at least I position selected from L49, H29, H30, H49 and H98 is occupied by the amino acid at the equivalent position of the MuVTml-1 antibody heavy or light chain variable region framework. Such humanized antibodies (see AXY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times frut of MuVTml-1. They are used for treating a patient suffering from, or at risk of, the toxic effects from a patient suffering cfor treating verotoxin producing Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized antibody binding to verotoxin II used for treating Verotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vasques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1; monoclonal antibody; light chain; mouse; humanised antibody; Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_except= (pos:184..186, aa:Lys)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse anti-verotoxin II antibody VTml-1 VL cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TELJ ) TELJIN LTD.
(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                        AAZ35242 standard; cDNA; 381 BP
                                       301 gggacaaacttggaaataaa 320
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                                                                                                                                                                                                                                                                                                                                                                                (first entry)
301 GGGACCAAGGTGGAAATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUS; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9959629-A1.
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Claim 1; Page 440; 803pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                           61 gatgttgtgctaactcagtctccagccacctgtctgtgactccaggagatagcgtcagt 120
                                                                                                                                                                                                                          CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                     121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
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                                    Gaps
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                                                                                            GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                             54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted expressed sequence tag SEQ ID NO:921.
   Pred. No. 7.4e-64;
                                                                                                                                 tumour; infection; depression; psoriasis; ss
                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA44346 standard; cDNA; 651 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 gggaccaagctggagctgaa 380
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82.58;
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                                 Matches 264; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merberg
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AAA AAA4326 to AAAA5925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic: chemotactic; proliferative; immunomodulatory; haematopoietic: chemotactic; analgesic; haemacstatic; thrombolytic; antidiabatic; corpostatic; antibacterial; antifundal; antiviral; antidiabatic; antidathmatic; vulnerary; antidice; osteopathic; neuroprotective; corportoric antiparkinsonian; antipsoriantic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length colons and genomic DNA condecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions of setoporosis, osteoarthritis, central nervous system disorders (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Cohn's parkinson's, Huntington's disease, stroke), coagulation disease), tumours, bacterial, fungal or viral infections, depression and soriasis. AAA45926 to AAA45921 represent invention.
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APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: CO, Man Sung

APPLICANT: CANDELDER, William P.

APPLICANT: CANDELT, Nicholas F.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES:

ADDRESSEE: Townsend and Townsend Khourie and Crew
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-SEP-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATFORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30,23
REGISTRATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....ureSEE: Townsend and Townsend Khourie and to STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                               US-09-042-353-41

US-08-053-131-180

US-08-096-762-180

US-09-042-353-43

US-09-042-353-43

US-09-042-572A-19

US-08-041-889-10

US-09-041-889-10

US-09-240-274-201

PCT-US93-12501-1

US-08-476-176B-9

US-08-485-246A-9

US-08-485-246A-9

US-09-240-274-216

US-09-240-274-216

US-09-240-274-107

US-08-476-176B-7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5530101
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US-08-232-081B-35
US-08-737-560A-13
US-08-737-560A-8
US-08-737-560A-8
US-08-737-560A-8
US-08-127-721A-3
US-08-127-721A-3
US-08-325-081B-39
US-08-326-595-3
US-08-800-198-7
US-09-296-595-7
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Minimum DB s Maximum DB s

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Result No.

Searched:

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                                                                                                                                                                                                                                                                                                     Length 381;
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APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UNMER: US/08/477,728
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                             Ouery Match 76.5%; Score 245.6; DB 1
Best Local Similarity 85.0%; Pred. No. 5.9e-70;
Matches 272; Conservative 2; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PULDA APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/310,252 FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 82, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GGGACCAAGCTGGAAATAAA 380
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                               MOLECULE TYPE: CDNA FEATURE:
   linear
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                                                                                                         ; NAME/KEY:
; LOCATION:
US-07-634-278-82
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-728-82
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61 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
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Patent No. 5693761

GENERAL INFORMATION:

APPLICANT: Co, Man Sung
APPLICANT: SCHNEIDER, William P.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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.9e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 245.6; D. Pred. No. 5.9e-2; Mismatches
                                                                                                 REFERENCE/DOCKET NUMBER: 11823-002600 TELECOMMUNICATION INFORMATION:
  us 07/290,975
                                                          NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GGGACCAAGGTGGAAATTAA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.5%;
ilarity 85.0%;
Conservative
                   FILING DATE: 28-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                               LENGTH: 381 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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Best Local Similarity
Matches 272; Conserv
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US-08-477-728-82
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61 CTTTCCTGCCAGCCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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Pred. No. 5.9e-70;
2; Mismatches 46; Indels
                                                                                                                                                             APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
UNDRER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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URENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

TOWN APPLICATION DATA:

APPLICATION NUMBER:

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NUMBER:

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APPLICATION NUMBER:

ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

APPLICATION NUMBER:

ATTORNEY/AGENT NUMBER:

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ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

ATTORNEY/AGENT NUMBER:

                                                                                                                                                                                                                                                                                      Townsend and Townsend and Crew
                                           CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTK1.

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATIBLE
POSTAGE
COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-242
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.5%;
Best Local Similarity 85.0%;
Matches 272; Conservative ;
                                                                                                                                                                                                                                                                                                            379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-487-200-82
                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GAAGATTTTGCAGTCTATTACTGTCAACAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGATTGTGTGTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 5.9e-70;
2; Mismatches 46; Indels 0
SOFTWARE: PC-DOS/MS-DOS
SUFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEC ID NO: 82:
                                                                                                                                                                                                                                        PRIOR APPLICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 82, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.5%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.59
Best Local Similarity 85.09
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1..381
US-08-474-040-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-487-200-82
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TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
                                                                                                                                                                                                                                     61 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
                                                                                                                              CTTTCCTGCCAGGCCAGACAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                   GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
    Gaps
                                             GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
                                                                                                                                                                                                                                                                                                                        GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC
                                                                                                                                                                                                                                                                                                AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT
    ö
    46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463 FILING DATE: 20-20N-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: BROWDY AND NEIMARK, P.L.L.C. 419 Seventh Street, N.W., Suite 400
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08436463 Patent No. 5760185
    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GGGACCAAGCTGGAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 424 base pairs
  Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Seve
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-436-463-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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241 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
                                                             301 GAAGATTTTGGAATGTATTTCTGTCAACAGAGTAACAGTTGGCTCATACGTTCGGAGGG 360
                                           241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 245.6; DB 4; Length 381; Pred. No. 5.9e-70;
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Rathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                US-08-484-537-82
Sequence 82, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
                                                                                                                                                                 361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                          301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.5%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-484-537-82
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61 CTTTCCTGCCAGCCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCCAGTCTGGAGCCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGATCGTCCTGACTCGTCGTCCACGCCACACTGTCTCTGAGTCCAGGAGAAGAGCCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCAGGAGAAAGGGCGACT 60
GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.0%; Score 224.8; DB 2; Best Local Similarity 80.9%; Pred. No. 2.7e-63; Matches 259; Conservative 2; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BIRCH, STEWART, KOLASCH AND BIRCH
PO BOX 747
                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                             Sequence 35, Application US/08232081B Patent No. 5886152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                 301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                   TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 321 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALLS CHURCH
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                            RESULT 8
US-08-232-081B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-081B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                     ; Patent No.
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                                                                                                                                                                                                                                                                                                                                          AGGITCAGTGGCAGTGGATCAGGGACAGATTICACCCTCACTATCTCCAGTCTGGAGCCT 240
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                                                                                                                                 Gaps
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Patent No. 5453363

TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR TITE GENERICESSION IN PROKARYOTES

ING AFTER GENERICE EXPRESSION IN PROKARYOTES

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,044

FILING DATE: 02-MAR-1994

APPLICATION NUMBER: 942,370

FILING DATE: 09-SEP-1992

APPLICATION NUMBER: 498,500

FILING DATE: 23-MAR-1996

APPLICATION NUMBER: 76,207

FILING DATE: 23-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5238;
                                                                                            Length 424;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                        Score 245.6; DB 1
Pred. No. 6.2e-70;
2; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.5e-67.
1; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 239.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 GGGACCAAGCTGGAGCTGAA 402
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84.1%;
                                                                                        Query Match 76.5%;
Best Local Similarity 85.0%;
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 84.1
Matches 269; Conservative
                 23..403
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NAME/KEY:
                   LOCATION:
                                   US-08-436-463-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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241 GAAGATTTCGCAGTCTATTACTGTCAACAAGTAGTAGCTGGCCGCTCACGTTCGGTCAG 300
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                                                                      GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KANG, Chang-Yuil
APPLICANT: KIM, Joong-Gon
TITLE OF INVENTION: 4.1BB AND CELL LINE PRODUCING SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 222; DB 2; Length 324;
Pred. No. 2.1e-62;
L; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: Kwanak-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotide encoding 4B4-1-1 light chain variable region
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COMPUTER READABLE FORM:
MEDTUM TYPE: DISKette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
COMPUTER: IBM PC/AT
COMPUTER: WAS "DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,560A
FILING DATE: 13-NOV-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08737560A Patent No. 5928893
                                                                                                                                                          301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                301 GGGACCAAGGTCGAGATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seoul
STATE: Seoul
COUNTRY: Republic of Korea
ZIP: 151-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.2%;
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APPLICATION NUMBER: KR 9:
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 324 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.65
Matches 258; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION:
US-08-737-560A-13
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                                                                                                                                                                                                                                                                    RESULT 10
US-08-737-560A-13
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181 AGGTTTAGTGGCAGTGGATCAGGGACAGATTTACTCTTACAATCTCCAGGCTGGAGCCA 240
                                                                                        6 CTGTCCTGCAGGGCCAGTCAGACCATTGGCACAAGCATACACTGGTATCAGCAGAGAGACCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: WIJDENES, JOHN
ITILE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.7%; Score 223.6; DB 2 larity 80.9%; Pred. No. 6.5e-63; Conservative 1; Mismatches 60
                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/08232081B Patent No. 5886152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
RECISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
                                                                                                                                                                                301 GGGACCAAGGTCGAGATAAA 320
                                                                                                                                                   301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 259; Conserv
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STATE:
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MOLECULE TYPE: DNA
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                                                              121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
                                                                                                                            181 AGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCTCACTATCTCCAGTCTGGAGCCT 240
                                                                                                                                                                                          GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                     APPLICANT: KANG, Chang-Yuil
APPLICANT: KIM, Joong-Gon
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
TITLE OF INVENTION: 4.1BB AND CELL LINE PRODUCING SAME
WUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: KIM, Joong-Gon
STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: KANG, Chang-Yuil
STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
STREET: Kwanak-gu
CITY: Seoul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 135-110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADJON 11.1.
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,560A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: RK 95-8176
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                   RY: Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                         1 to 324 bp 4B4-1-1 light chain variable region 70 to 102 bp hypervariable region CDR1 4B to 168 bp hypervariable region CDR2 255 to 291 bp hypervariable region CDR3 325 to 363 bp 4B4-1-1 light chain constant region
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APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Immunoglobulin isotype
                                                                                                                                                                                                                                                  Length 363;
                                                                                                                                                                                                                                                     Score 222; DB 2; Length 36
Pred. No. 2.2e-62;
1; Mismatches 61; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
CORRESSED: Nq. 5598708artis Patent Department STREET: 59 Route 10
CITY: Bast Hanover STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PULLOATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION UNBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                     69.2%;
80.6%;
                                                                                                                                                                                                                                                                              Best Local Similarity 80.6
Matches 258; Conservative
FEATURE:

OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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CURRENT APPLICATION DATA:
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Patent No. 6066718
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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CITY: E35H Hanover: STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                            /product- "light chain variable domain of murine antibody TES-C21"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                            66.5%; Score 213.6; DB 2
78.8%; Pred. No. 1.1e-59;
                                      4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
NAME: NO. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-1927
TELECOMUNICATION:
TELECOMUNICATION:
TELEPAN: (908) 277-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GGGACCAAGCTGGAGATAAA 320
                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                252; Conservative
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-476-176B-3
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Matches 252; Conserv
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61 TICTCCTGCAGGGCCAGTCAGAGCATTGGCACAAACATACACTGGTATCAGCAAAGAACA 120
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APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.5%; Score 213.6; DB 3; Length 322;
nilarity 78.8%; Pred. No. 1.1e-59;
Conservative 2; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "light chain variable domain of murine antibody TES-C21"
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                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25.SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION UNBER: 33,200
REFERENCE/DOCKET NUMBER: 4.19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
SEQUENCE CHARACTEISTICS:
US/08/127,721A
                   27-SEPTEMBER-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1.321
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 252; Conserv
                      FILING DATE: 27 CLASSIFICATION:
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NAKATANI, TOMOYUKI

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Search completed: October 11, 2001, 15:14:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "light chain variable domain of murine antibody TES-C21"
                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
                                                                                                                                                                                     PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NAMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTOMNEX/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REGISTRATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/08232081B Patent No. 5886152 GENERAL INFORMATION:
                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GGGACCAAGCTGGAGATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGACCAAGGTGGAAATTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 322 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.59
Best Local Similarity 78.89
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1.321
OTHER INFORMATION:
OTHER INFORMATION:
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                07936-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                             FILING DATE:
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US-08-232-081B-39
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121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCCAGTCCATCTCTGGGATCCCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCGGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGGTATCAACAAAGGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGATTGTGCTAACTCCAGTCTCCAGCCACCTGTCTCTCAGCCCAGGAGAAGGGCCGACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 204; DB 2; Length 321; 76.9%; Pred. No. 1.3e-56; ive 2; Mismatches 72; Indels
                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYETEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                       ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
APPLICANT: GONI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: WOGOCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEGONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGACCAAGCTGGAGCTGAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-232-081B-39
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Job time: 5003 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 11, 2001, 12:02:36; Search time 31.63 Seconds (without alignments) 257.688 Million cell updates/sec Run on:

US-08-791-391A-32 557 1 EIVLTQSPATLSLSPGERAT......CQQSGSWPHTFGGGTKVEIK 107 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 68:* Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	470	84.4	144	5	PL0106	Iq kappa chain pre
7	460	82.6	111	7	S23628	kappa chain
ю	458	82.2	128	~	A56701	kappa
4	457	82.0	128	N	S40379	kappa
Ŋ	452.5	81.2	114	~	S54905	kappa
9	451	81.0	108	ď	G44151	Ig kappa chain V r
7	447	80.3	106	~	PC4282	Ig kappa chain (an
80	447	80.3	107	N	B45722	i-glyc
O	444	79.7	117	7	S40362	Ig kappa chain - h
10	443	79.5	125	~	S40344	g kappa
11	442	79.4	123	N	S35479	Ig kappa chain pre
12	441	79.2	107	~	A45722	nti-glycoprote
13	440.5	79.1	109	7	A30608	Ig kappa chain V-I
14	440	79.0	129	~	S29627	
15	. 438	78.6	128	~	S40345	
16	437	78.5	107	7	S34005	
17	436	78.3	106	7	PL0267	
18	433.5	77.8	108	7	B30608	
19	433.5	77.8	129	~	A32274	
20	432.5	77.6	109	7	G30607	kappa chain
21	431.5	77.5	109	٦	K3HUTI	
22	431	٠	107	~	S57444	
23	430.5	•	109	7	D30601	
24	430.5	77.3	109	~	C30601	
25	429.5	•	109	N	н30601	
56	429	7	128	7	S40343	
27	28	76.9	109	Н	K3HUSI	
28	427.5	76.8	109	7	G30601	kappa
59	427.5	76.8	109	7	B30601	

kappa chain	ig kappa chain pre Ig kappa chain NIG	kappa chain	kappa chain	anti-Sm antibody V	Ig kappa chain v r	Ig kappa chain V-I	Ig kappa chain V-I	Ig kappa chain pre	Ig kappa chain V-J	Ig kappa chain - h	Ig kappa chain pre	Ig kappa chain V-I	IG light chain var	Ig kappa chain V r
\$20636	JE0244	C30608	S20635	S49532	PH0963	F30607	K3HUWL	K3HUHI	S46375	S40360	A26471	F30601	S46369	538643
7	- 7	7	~	~	~	~	-	Н	~	~	~	7	7	7
128	215	108	110	129	109	109	109	129	114	130	138	109	129	134
76.8	76.6	76.4	76.2	76.2	76.0	0.94	75.9	75.9	75.4	75.3	75.2	75.0	75.0	75.0
427.5	426.5	425.5	424.5	424.5	423.5	423.5	422.5	422.5	420	419.5	419	417.5	417.5	417.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT PL0106

PUBLION
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Journisps #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C; Accession: PLO106
R; Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 163-11643, 1989
A; Title: Relationship of variable region genes expressed by a human B cell lymphoma s
A; Reference number: PLO106; MUID: 89235583
A; Accession: PLO106
A; Molecule type: mRNA
A; Residues: 1-144 <SIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <IMM>F; 1-20/Domain: immunoglobulin homology <IMM>F; 1-21/Domain: immunoglobulin homology <IMM>F; 36-110/Domain: immunoglobulin homology <IMM>F; 44-54/Region: complementarity-determining 2
F; 109-115/Region: complementarity-determining 3
F; 116-127/Domain: J region (fragment) <CRE>
F; 128-144/Domain: C region (fragment) <CRE>

Gaps ö Length 144; 84.4%; Score 470; DB 2; Length 14 85.0%; Pred. No. 1.4e-34; ive 6; Mismatches 10; Indels Query Match
Best Local Similarity 85.0
Matches 91; Conservative

ö

1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPCQAPRLLIXYRSQSISGIPA 60 ò

21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLLIYDASNRATGIPA 80 g

61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107 q à

Ig Kappa chain V region - human (fragment)

[G Species: Homo sapiens (man)

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Ig kappa chain V region (JM-10) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C; Jaccession: G44151
R; Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A; Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A; Reference number: A44151; MuID:92228746
A; Accession: G44151
                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S54905
R;Esposito, G: Traboni, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PID:g809555 Cs.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin compley rine; F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB: M88317; NID:g183968; PIDN:AAA35975.1; PID:g183969
A;Note: nucleotide translation not given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>
                                                                                     EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Esposito, G.; Traboni, C.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and Sequencing of cDNA coding for the variable of A;Reference number: S54905
A;Accession: S54905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 108;
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                             Indels
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                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                81 RFSGSGAGTDFTLTISSLEPEDFAVYYCQQRSKWPWTFGQGTKVEIK 127
                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.2%; Score 452.5; DB 2;
80.6%; Pred. No. 3.8e-33;
:ive 11; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

81.0%; Score 451; DB 2;
Best Local Similarity 82.7%; Pred. No. 4.9e-33;
Matches 86; Conservative 8; Mismatches 10
  1.7e-33;
                             Mismatches
  Pred. No.
                             7;
81.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.2%
Best Local Similarity 80.6%
Matches 87; Conservative
Best Local Similarity 81.39
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-114 <ESP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C) Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C; Accession: A56701
R; Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A; Title: Human and mouse monoclonal antibodies to blood group A substance, which are IA; Reference number: A56701; WUID:95279371
A; Reference number: A56701
A; Maccession: A56701
A; Residues: L-128 < NIC>
A; Residues: 1-128 < NIC>
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C. Species: Homo sapiens (man)
C. Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C. Accession: $40379
E. M. J. Immunol. 23, 3248-3371, 1993
E. M. J. Immunol. 23, 3248-3371, 1993
A. Title: Expressed human immunoglobulin chi genes and their hypermutation.
A. Accession: $40379
A. Status: preliminary; translation not shown
A. Molecule type: mRNA
A. Residues: 1-128 <KLE>
Cross-references: EMBL:X59705; NID:q34022; PIDN:CAA42226.1; PID:q1335190
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                     1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L41174; NID:9762823; PIDN:AAA64877.1; PID:9762824 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                        Length 111;
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                          C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.2%; Score 458; DB 2; Length 12
Best Local Similarity 82.2%; Pred. No. 1.4e-33;
Matches 88; Conservative 8; Mismatches 11; Indels
                                                                                                                                                                                                                             7; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region precursor (HuA) - human (fragment)
                                                                                                                                                                     Score 460; DB 2;
Pred. No. 8.1e-34;
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                                                                                                                                                                     82.6%;
83.2%;
                                                                                                                                                               Query Match
Best Local Similarity 83.28
Matches 89; Conservative
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61 81

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Query Match

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Ig kappa chain - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Accession: S40362
R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: S40312; MUID: 94080891
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Status: 1-117 < KLE>
A; Cross-references: EMBL: X72472; NID: 9441412; PID: 9441413
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 26-100/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-May.1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Date: 19-May.1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Date: 10-May.1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: S40312; MUID:9408091
A; Reference number: S40312; MUID:9408091
A; Accession: S40344
A; Residues: I-125 < KLE>
A; Cross-references: EMBL: X72454; NID:9441376; PIDN:CAA51122.1; PID:9441377
C; Superfamily: Immunoglobulin homology cIMM>
F; 36-110/Pomain: immunoglobulin homology < IMM>
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S35479
IG kappa chain precursor V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: J997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.7%; Score 444; DB 2;
llarity 79.4%; Pred. No. 2.2e-32;
Conservative 11; Mismatches 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V-J region - human
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Matches 85; Conserv
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                                                                                                                                                                            Ig Kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: PC4282; PC4284
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
A;Title: Molecular cloning of anti-ss-A/Ro 60-Kba peptide fab fragments from infiltratin A;Reference number: PC4279; MUID:97236289
A;Accession: PC4282
A;Molecule type: protein
A;Residues: 1-106 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjoeg C;Superfamily: immunoglobulin V region; immunoglobulin homology F;14-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                         GSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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ilarity 81.0%; Pred. No. 1.1e-32;
Conservative 10; Mismatches 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A45722; MUID:93100833
A; Accession: B45722
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Best Local Similarity 75.7%
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 1-106 <SU2>
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Matches 85; Conserv
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A; Note: E-56
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A, Accession: S40345
A, Status: preliminary; translation not shown
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79.8%; Pred
7; 1
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81.5%;
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Best Local Similarity
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Matches 87; Conserv
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                                    A;Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from A;Reference number: S35479; MUID:92375706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Specides: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A4572
C:Accession: A4572
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites can be a preliminary; not compared with conceptual translation
A;Reference number: A45722; MUID:93100833
A;Accession: A45722
A;Status: preliminary; not compared with conceptual translation
A;Rederence type: mRNA
A;Residues: 1-107 <SIM>A;Note: sequence extracted from NCBI backbone (NCBIP:120589)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: glycoprotein
F;16-90/Domain: immunoglobulin homology <INM>
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A; Residues: 1-123 <TAK>
A; Residues: 1-123 <TAK>
A; Residues: 1-123 <TAK>
A; Residues: 1-123 <TAK>
A; Residues: 1-124
A; Residues: 1-124
B; Rightion: 6
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Regiverds: heteroterramer; immunoglobulin #status predicted <SIG>
F; 1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F; 1-12/Domain: immunoglobulin N region (fragment) #status predicted <MAI>
F; 28-102/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match
79.2%; Score 441; DB 2; Length 10
Local Similarity 73.8%; Pred. No. 3.6e-32;
nes 79; Conservative 18; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                       79.4%; Score 442; DB 2; Le
74.8%; Pred. No. 3.4e-32;
iive 18; Mismatches 9;
                                                                             A;Accession: S35479
A;Status: nucleic acid sequence not shown
  Hoffman, R.W.
R; Takeda, Y.; Wise, K.S.; Hoffman,
Nucleic Acids Res. 20, 4099, 1992
                                                                                                                                                                                                                                                                                                                                                       Query Match 79.4%
Best Local Similarity 74.8%
Matches 80; Conservative
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Best Local Si
Matches 79,
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A;Title: Structural and idiotypic characterization of the L chains of human IgM autoa A;Reference number: A30601; MUID:89215279
A;Recession: A30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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Ig kappa chain V region (60.3 hybridoma) - human
Ig kappa chain V region (60.3 hybridoma) - human
Is kappa chain so man say librarias (man)
Is pare to 6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
Is Accession: S34110; S29627
Is Walls, M.A.; Helao, K.; Harris, 1.J.
Nucleic Acids Res. 21, 2921-2929, 1993
A; Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
A; Reference number: S34110; MUID:99324379
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-129 < WALZ>
A; Residues: 1-129 < WALZ>
A; Residues: Information for the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to the pare to th
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A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cel
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Genetics:
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C.Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.C.Accession: 840345
R.K.Lein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 36-110/Domain: immunoglobulin homology <IMM>
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Pred. No. 5.3e-32;
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Pred. No. 4.1e-32;
7; Mismatches 12
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A;Molecule type: mRNA
A;Residues: 1-128 <KLE>
A;Cross-references: EMBL:X72455; NID:g441378; PIDN:CAA51123.1; PID:g441379
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>
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ï 2; Gaps Query Match

78.6%; Score 438; DB 2; Length 128;
Best Local Similarity 78.9%; Pred. No. 7.9e-32;
Matches 86; Conservative 8; Mismatches 13; Indels g õ

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61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPH--TFGGGTKVEIK 107

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Search completed: October 11, 2001, 12:02:36 Job time: 301 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:08:43; Search time 17.83 Seconds

(without alignments)

205.571 Million cell updates/sec
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01622 homo sapien) homo	homod	рошо	homo	homo	homod	homo	homo	homo	homo	homo	рошо	mus m	P80362 homo sapien	mus m	P01670 mus musculu	homo	homo	homo	homo	рошо	рошоц	2 mus m	рошо	P06313 homo sapien	mus m	Bus	P01625 homo sapien	mus m	P01599 homo sapien	P01665 mus musculu	P01606 homo sapien
SUMMARIES	ID	KV3D_HUMAN	KV3B_HUMAN	KV3L_HUMAN	KV3E_HUMAN	KV3M_HUMAN	KV3H_HUMAN	KV3I_HUMAN	KV3F_HUMAN	KV3A_HUMAN	KV3K_HUMAN	KV3G_HUMAN	KV1M_HUMAN	KV1H_HUMAN	KV3H_MOUSE	KV1Y_HUMAN	KV3L_MOUSE	KV3R_MOUSE	KV3J_HUMAN	KV1W_HUMAN	KV1E_HUMAN	KV3C_HUMAN	KV1P_HUMAN	KV1V_HUMAN	KV5I_MOUSE	KV4C_HUMAN	KV4B_HUMAN	KV3J_MOUSE	KV3T_MOUSE	KV4A_HUMAN	KV3U_MOUSE	KV1G_HUMAN	KV3M_MOUSE	KV1N_HUMAN
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ALIGNMENTS

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		Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	DECUENCE. MEDLINE=72188439; PubMed=5027703; Suter L., Barnikol H.U., Watanabe S., Hilschmann N.; "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of Kappa-type, subgroup 3 (Bence-Jones prot Timmunoglobulin L-complete annino acid sequence and its significance for	r production."; Chem. 353.189-208(1972). REGION OF THIS CHAIN HAS THE INV (3). MARKER. S A BENCE-JONES PROTEIN.	**	Length 109; Indels 1	EIVLTOSPATLSLSPGERATLSCQASQSISN-HLHWYQQRPGQAPRLLIXYRSQSISGIP 	107	¢	
		Craniata; Vertebrata; Eutel Catarrhini; Hominidae; Homo	nann N.; ucture of up 3 (Ber 1 its siq	(1972). N HAS THE FEIN.	Johnes Procein. SIMILARITY. 8C35O58CDC7749BC CRC64;	DB 1; Len :-38; 15; Ind	RPGQAPRLI : KPGQAPRLI	ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTPGGGTKVEIK		
AA.	te) date	Verte ; Hor	lschr stri bgrou	-208 CHAII PRO	ry.	5; DB 1 3.2e-38; thes 15	100 AV	PHTF(A.A.	te) Jate
109	upda:	ta; ¹ hini	, Hi nary , sul	:189 :189 HIS (LARI SBCD	31.5 5.3 atch	- HLHI - SFLAI	SGSWI - YGSSI	109 AA	upda1 n upc
PRT;	01, Created) 01, Last sequence update) 38, Last annotation update)		7703; anabe S. The prin ppa-type	oduction hem, 353 ION OF TI BENCE-JO	BY	Score 431.5; Pred. No. 3.2d 5; Mismatches	DASQSISN:	FAVYYCQQ! 	PRT;	Created) Last sequence update) Last annotation update) RGION SIE.
.RD;	886 (Rel. 01, Created) 886 (Rel. 01, Last sequ 999 (Rel. 38, Last anno CHAIN V-III REGION TI.	Chordata; Primates;	PubMed=5027703; LH.U., Watanabe structure. The chain of Rappa-t	Lbody prosition of the control of th		77.5%; 80.6%; ive	ERATLSC(SSLEPEDI SRLEPEDI	.RD;	
STANDARD;	(Rel. 01, (Rel. 01, (Rel. 38, IN V-III F	ens (Human). ; Metazoa; C Eutheria; P D=9606;	139; Pub likol H. body str n L-chai	of anti s Z. Phy sous: TH sous: TH canuri. 2MCP.	AA;	77. larity 80. Conservative	ATLSLSPG STLSLSPG	STDFTLTI 	STANDARD;	
z	36 (F 36 (F 39 (F	ens ; Met Eut} D=96(21884 Barr antik	LLLANI LLLANI LLLANI 95; P 789; IPR(100	imilā ; CC	TOSP?	38686 38686	z	36 (F 36 (F 39 (F
HUMAN KV3D_HUMAN P01622:	51514	Homo sapiens (Human) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	SEQUENCE. MEDLINE=72188439; PubMed=5027703; Suter L., Barnikol H.U., Watanabe S., Hilschmann Immunod antibody structure. The primary structure immunoglobulin L-chain of kappa-type, subgroup 3 (71). If the complete amino acid sequence and its	the mechanism of antibody production."; Hoppe-Seyler's Z. Physiol. Chem. 333:189-208(1972) HOPPE-SEYLER'S Z. Physiol. Chem. 333:189-208(1972) HIS MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS PIR, A01895; KAHUTI. HSSP, P01789; 2MCP. HIGEPPO, IPRO03006; Pfam, PF00047; 19; 1.	INMARIOGICELLI DISULFID 23 NON_TER 109 SEQUENCE 109	ದ ೮	1 EIVL EIVL	60 ARFSC 61 DRFSC	T 2 HUMAN KV3B_HUMAN P01620;	21-JUL-1986 (Rel. 01 21-JUL-1986 (Rel. 01 15-JUL-1999 (Rel. 38 IG KAPPA CHAIN V-III
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Matches 86; Conserv
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P01623;
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KV3M_HUMAN
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                                                                                                  -I: MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
HSSP; P01789; ZMCP.
InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
                                                 Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idlotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                     Gaps
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
BY SIMILARITY.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                        61 DRFSGSGGTDFTLTISRLEPDDFAVYCQQYGSSPQTFGGGSKVEIK 108
                                                                                                                                                                                                                                                                                                              60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                                                                                                                                                                                            76.9%; Score 428.5; DB 1; ilarity 79.6%; Pred. No. 6.6e-38; Conservative 7; Mismatches 14;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 18, Last annotation update)
1G KAPPA CHAIN V-III REGION HAH PRECURSOR.
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                                        MEDLINE-82046598; PubMed-6794615;
                                                                                           Biochemistry 20:5816-5822(1981)
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 86; Conserv
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         NCBI_TaxID=9606;
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P18135;
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Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
PIR: A01896; K3HUWL.
HSSP; P01789; 2MCP.
InterPro; IPR003006; -
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                     Gaps
                                                                                                                                                                                         1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQQRPGQAPRLLIXYRSQSISGIP 59
                                                                                                                                                                                                                     21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPQQAPRLLIYGASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                            Length 129;
                                                                                                                                                                                                                                                                                                                              61 DRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGSLGRTFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                                  60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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                                                                                                                                  Indels
14073 MW; D3C55292772774D0 CRC64;
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11746 MW; 566C115E6B9CBEEE CRC64;
                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-MAPA CHAIN V-III REGION WOL.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 APPA CHAIN V-III REGION HIC PRECURSOR.
Homo sapiens (Human)
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                                                                                                         Best_Local Similarity 79.6
Matches 86; Conservative
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KV31_HUMAN
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                  MEDLINE-88171307; PubMed=3127527; Ripps T.J., Tomhave E., Chen P.P., Carson D.A.; Ripps T.J., Tomhave E., Chen P.P., Carson D.A.; Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Inplications for etiology and immunotherapy."; mutation. Implications for etiology and immunotherapy."; J. Exp. Med. 167:840-852 (1988).
                                                                                                                                                                                                                                                                                                                                                                                           1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQQRPGQAPRLLIXYRSQSISGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-86177570; PubMed=3083417;
Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
                                                                                                                                                                                                                                                                                                                                                75.9%; Score 422.5; DB 1; Length 129; 79.6%; Pred. No. 3.4e-37; tive 6; Mismatches 15; Indels 1
                                                                                                                                                                                                     IG KAPPA CHAIN V-III REGION HIC
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                                                                                                                                                                                                                                                                                                                14070 MW; 7395528EA2BB74D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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HSSP; P01789; 2MCP.
InterPro; IPR003006; -.
Pfam; PF00047; ig; i.
Immunoglobulin V region; Signal.
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129 AA;
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NCBI_TaxID=9606;
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                                                                                                                         LEUKEMIA.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVLTOSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pech M., Zachau H.G.; "Immunoglobulin genes of different subgroups are interdigitated
                                                                                                                                                               IG KAPPA CHAIN V-III REGION CLL. FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 129;
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COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSW-PHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                             5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                        FRAMEWORK 3.
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Nucleic Acids Res. 12:9229-9236(1984).
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PIR; A01900; K3HUVG.
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Pfam, PF00047; ig; 1.
Immunoglobulin V region; Signal.
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                                                InterPro; IPR003006; -. Pfam; PF00047; 1g; 1. Immunoglobulin V region
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PIR; A01898; K3HUCL.
HSSP; P01789; 2MCP.
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            NCBI_TaxID=9606;
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                                      Milstein C.;
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P06311;
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"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Paris) 127C.261-271(1976).
--I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACIVITY.
PIR: A01897; K3HUPM.
HSSP: P01789; 2MCP.
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                                                                                            1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
IG KAPPA CHAIN VIT REGION POM.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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  COMPLEMENTARITY-DETERMINING 3. BY SIMILARITY.
                                                       Length 115,
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                            12575 MW; 2DE47CDA3A17D555 CRC64;
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                                                       Score 413; DB 1; L. Pred. No. 2.9e-36; 7; Mismatches 9;
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ID KV3A_HUMAN

STANDARD; PRT; 108 AA.

AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
                                                                                                                                          61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWP 95
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                                                       74.18;
83.28;
                                                   Query Match
Best Local Similarity 83.2%
Matches 79; Conservative
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Immunoglobulin V region.
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Best Local Similarity
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                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASOSIS-NHLHWYQQRPGQAPRLLIXYRSQSISGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-III REGION IARC/BL41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DRFSGSGSGADFTLTISRLZPEDFAVYXCQQXGSSPFTFGGGSKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 406.5; DB 1; Length
; Pred. No. 1.3e-35;
12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JNN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
                                                                                                                                                                                                                                                               128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z00021; CAA77316.1; -. PIR; A01899; K3HU41.
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Best.Local Similarity 73.1%;
Matches 79; Conservative 1:
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COMPLEMENTARITY - DETERMINING 1.
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11834 N
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PIR, A01871; K1HULY.
HSSP; P01607; IREI.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                              68; Conservative
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23
108
108 AA;
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Best Local Similarity
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NON_TER
SEQUENCE
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KV1H_HUMAN
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Matches
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Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Namino acid sequence of a light chain variable region of a human
rheumatoid factor of the wa idiotypic group, in part predicted by its
reactivity with antipeptide antibodies.";
Mol. Immunol. 23:239-244(1986).
HSSP: P01789; ZMCP.
HSSP: P01789; ZMCP.
InterPro; IPRO30006; -.
Pfam: PF00047; ig. 1.
Immunoglobulin V region.
                                                                                            Gaps
                                                                                                                 1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                               21 EIVLTQSPGTLSLSPGESATLSCRASQSVSSNLAWYQQKRGQSPRLLIRDASSRANGIPD 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-I REGION LAY.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                      Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                            17; Indels
                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                  14070 MW; CC8957F0FE3B9012 CRC64;
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                                                                    72.9%; Score 406; DB 1;
74.8%; Pred. No. 1.7e-35;
iive 10; Mismatches 17
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 JK1 SEGMENT.
BY SIMILARITY
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                                                                                            80; Conservative
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118 1
43 1
128 1
                                                                                Similarity
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P04206;
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P01605;
                                                                     Query Match
Best Local S:
Matches 80
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SEQUENCE
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            DISULFID
                                   SEQUENCE
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Matches 8
                        NON_TER
 DOMAIN
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Scand. J. Immunol. 5:677-684(1976).
-1- MISCELLANDOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (3) MARKER
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MEDLINE=77038198; PubMed=824717; Capra J.D., Klapper D.G.; Capra J.D., Klapper D.G.; Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-71032830; PubMed-4097974;
Watanabe S., Hilschmann N.;
"The primary structure of monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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63.6%; Pred. No. 7.1e-33;
1ive 21; Mismatches 18
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 AAPPA CHAIN V-I REGION HAU.
HOmo sapiens (Human)
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MEDLINE-79012520; PubMed-99744;

MCKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-I- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL. PIR; A01934; KVMS37.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                               1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                COMPLEMENTARITY - DETERMINING 2.
                              FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                          Length 108;
                                                                                                                                       67.0%; Score 373; DB 1; Length 10 ilarity 65.4%; Pred. No. 3.8e-32; Conservative 20; Mismatches 17; Indels
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                                                                                                 08D3A6160D8D0618 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
                                                                                                                                                                                                                                                                                                                                                       111 AA.
                                                                       SIMILARITY.
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MEDLINE=79073152; PubMed=103003;
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11671 MW;
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Nature 276:785-790(1978).
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Best Local Similarity
Matches 70; Conserv
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P01660;
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DISULFID
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SEQUENCE
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Gaps
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                                                                                                                                                                                                                              MEDLINE-95086080; PubMed-7993911;
Mand D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
"Comparison of crystal structures of two homologous proteins:
"Structural origin of altered domain interactions in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            61 GIPARFSGSGSRTDFTLTINDVEADDVATYYCQQSNEDDYTFGGGTKLEIK 111
57 GIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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Pred. No. 7.7e-32;
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                                                                                                                                                                                                                     SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
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TN -> SD (IN REF. 2).
                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                   108 AA
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21; Mismatches
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63.6%;
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1 EIVLTQSPATLSLSPGERAT......CQQSGSWPHTFGGGTKVEIK 107
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9u185 homo sapien	Q9ul83 homo sapien	Q9ul78 homo sapien	Q9u186 homo sapien	Q9ul77 homo sapien	Q9ul79 homo sapien	Q9ul70 homo sapien	Q9ul81 homo sapien	Q9u410 schistosoma	Q9j174 mus musculu	Q9j184 mus musculu	Q9qyf0 mus musculu	Q9rla5 mus musculu	Q9j178 mus musculu	Q9erz9 mus musculu	Q91180 mus musculu	Q9j176 mus musculu	Q9u180 homo sapien	Q9j182 mus musculu
SUMMARIES	ID	Q9UL.85	Q9UL83	Q9UL78	O9UL86	Q9UL77	09UL79	Q9UL70	Q9UL81	Q9U410	Q9JL74	Q9JL84	Q9QYF0	O9R1A5	Q9JL78	Q9ERZ9	Q9JL80	Q9JL76	Ø90L80	Q9JL82
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61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPH-TFGGGTKVEIK 107

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O900w5 oryctolagus O9u182 homo sapien O9nsd6 homo sapien O9n524 homo sapien O91524 homo sapien O91524 homo sapien O61243 mus musculu O9u456 homo sapien O61243 mus musculu O9u456 homo sapien O91b00 sphoeroides O91b00 sphoeroides O91b00 sphoeroides O94b01 sphoeroides O94b01 ginglymosto O77624 bos taurus O99h11 ginglymosto O77624 bos taurus O99h11 ginglymosto O97624 homo sapien O99h12 ginglymosto O97767 mus musculu O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto O99h19 ginglymosto	AA. a update) ton update) ton update) ton update) ton update) ton update) ton update) to nupdate) to nupdate) to nupdate to nupdate to nupdate to nupdate to nupdate to nupdate to nupdate to numal to	tch al Similarity 78.7%; Score 429.5; DB 4; Length 109; al Similarity 78.7%; Pred. No. 7.1e-41; 85; Conservative 10; Mismatches 12; Indels 1; Gaps 1; EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
6 0900W5 4 090L82 4 090ET13 4 09NED6 4 09NE24 4 09H24 4 09H26 4 09H26 13 091B00 13 091B00 13 091B00 13 091B00 11 09WTN4 11 09WTN4 12 09WTN4 13 09YH19 13 09YH19 13 09YH19 13 09YH19 13 09YH26 13 09YH26 13 09YH26 13 09YH26 13 09YH26 14 09UL89	LIGNMENT: T; 109 sequence annotati aniata; \text{Arrhini}; tarrhini; \text{Kalis} in rheume 184-192(1) N AND MA.	%; Score 429.5; %; Pred. No. 7.1e 10; Mismatches LSCQASQSISNHLHWYQO LSCQASQSISNHLHWYQO LSCQASQSISSNLHWYQO LSCQASQSISSNLAWYQO
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                  1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQQRPGQAPRLLIXYRSQSISGIP 59
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                         Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                             60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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Pred. No. 1.2e-40;
6; Mismatches 14
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80.6%;
         InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                               87; Conservative
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InterPro; IPR003596; -.
Pfam; PF00047; 19; 1.
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109 AA;
 HSSP; P01789; 1MCP
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01-MAY-2000 (TTEWBLrel. 13, Last sequence update)
01-MAR-2001 (TTEWBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                             Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.8%; Score 428; DB 4; Length 108; Best Local Similarity 76.6%; Pred. No. 1e-40; Matches 82; Conservative 12; Mismatches 13; Indels
61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108
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MEDLINE-98277139; PubMed~9614934;
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HSSP; P01607; 1REI.
InterPro; IPR00306; -
InterPro; IPR003596; -
Ffam; PP00047; 19; 1.
SMART; SM00406; IGV; 1.
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UL81;
                                                                                                                                                                                              Q9UL70
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                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
         ol-mar-zoud (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGEOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98277139; Pubmed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                            69.1%; Score 385; DB 4; Length 108;
69.2%; Pred. No. 7e-36;
ive 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
                                                                                                                                                                                                   EMBL; AF035037; AAD56273.1; -. HSSP; P01607; 1REI. InterPro; IPR003306; -. InterPro; IPR003596; -. Ffam; PF00047; 19; 1. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF035035; AAD56271.1; -. HSSP; P01607; 1REI.
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                  74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SMART; SM00406; IGV; 1.
NON TER 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
WYOSIN-REACTIVE IMMUNGLOBULIN LICHT CHAIN VARIABLE REGION (FRAGMENT).
                                                       Gaps
                                                                                                      1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                  0; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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     DB 4; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.7%; Score 366; DB 4; Length 10 Best Local Similarity 64.5%; Pred. No. 9.5e-34; Matches 69; Conservative 17; Mismatches 21; Indels
                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B7BEDC3E41FCCA37 CRC64;
66.8%; Score 372; DB 4; Lv
llarity 67.3%; Pred. No. 2e-34;
Conservative 14; Mismatches 21;
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11633 MW;
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SMART; SM00406; IGV; 1
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FRAIN-BALB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
ENBL: AF206032; AAF69330.1; -.
InterPro; IPR03006; -.
Pfam; PF00047; ig; 1.
SNART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                 1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                   11 LSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPARFSGSGSGTD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MXOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TERMBLE). 15, Last sequence update)
01-MAR-2001 (TERMBLE). 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                              19; Indels
                                                                               61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA; 10939 MW; 3B25D0E784533324 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.0%; Score 334; DB 11;
61.9%; Pred. No. 3.4e-30;
iive 18; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 FTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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63 FTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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NON_TER
SEQUENCE
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Q9JL84
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Q9JL74
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                             1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MONOCLONAL ANTI-IDIOTYPE ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.; "Amplification, cloning and sequence analysis of the light chain variable region gene of monoclonal anti-idiotypic antibody NP30 _{\odot}
                                                                            Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                 ;;
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                                                                                                                                                                                                                                                                                                                                 65.1%; Score 362.5; DB 4; Length 107; 66.4%; Pred. No. 2.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 106;
                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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                                                                                                                                                                                                                                                                                   11501 MW; 070549FDE0754748 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA.
                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
             SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF207620; AAF19434.1; -. HSSP; P01679; 2FBJ. InterPro; IPR000308; -. InterPro; IPR003596; -.
                                                                                                                                                      EMBL; AF035033; AAD56269.1;
HSSP; P80362; 1WTL.
InterPro; IPR003006; -.
InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 66.48 Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.8
Best Local Similarity 59.8
Matches 64; Conservative
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SMART; SM00406; IGv; 1.
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ProDom; PD000600; -; 1.
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107 AA;
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                                                             Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schistosoma
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SEQUENCE
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SEQUENCE
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A SEQUENCE FROM N.A.

A Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;

"Cloning of cDNas encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";

Submitted (NAY-1999) to the EMBL/GenBank/DDBJ databases.

REMBL, AFI52371; AAD40242.1; -..

REMBL, AFI52371; AAD40242.1; -..

RESP: PO1789; IMCP.

RESP: PRO30006; -..

PRO3003006; -..

PRO30047; ig; 2.

RESP: PRO0490; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A.CA;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF206028, AAF69326.1;
InterPro; IPR0033006;
InterPro; IPR003596;
InterPro; IPR003596;
SMART; SM04406; IGV; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09JL78 PRELIMINARY; PRT, 101 AA.
09JL78;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNGELOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52BA205FDE995E2A CRC64;
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         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.4%; Score 331; DB 11; I Best Local Similarity 55.1%; Pred. No. 1.8e-29; Matches 59; Conservative 25; Mismatches 23;
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62.0%; Pred. No. 2.8e-29;
iive 16; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                     214
: 23922 MW;
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Best Local Similarity 62.0%
Matches 62; Conservative
                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA;
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SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
"method,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                      1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                              29; Indels
                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB036341; BAA88633.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; -.
InterPro; IPR003596; -.
Pfam; PF00047; ig; 2.
SMART; SMO406; igv; 1.
SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;
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Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                    107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                          60.0%; Score 334; DB 11;
58.9%; Pred. No. 3.7e-30;
ive 15; Mismatches 29;
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InterPro; IPR003596; -.
                       SMART; SM00406; IGv; 1.
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Best Local Similarity
Matches 63; Conserv
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Sequence FROM N.A.

A Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

A Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

RT "Cloning and sequencing of the light chain fragment of variable region grades of an anti-hTNR-a monoclonal antibody.";

RL J. Cell. Mol. Immunol. 12:21-26(1996).

RN [2]

RN Cell. Mol. J. Wang Z.L., Han H., Yao L.B., Su C.Z.;

RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

RT "Construction and sequencing of the single-chain antibody gene of a human TNF-alpha specific monoclonal antibody.";

RT Human TNF-alpha specific monoclonal antibody.";

RL J. Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                    10 TLSLSPGERATLSCQASQSI-SNHLHWYQQRPGQAPRLLIXYRSQSISGIPARFSGSGSG 68
                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
MAUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutenia; Rodentia; Sciurognathi; Muridae; Musinellarall-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.2.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF262753; AAG23804.1; -. NON_TER 107 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11784 MW; 2B15EEA6604A26C3 CRC64;
                                                                           69 TDFTLTISSLEPEDFAVYYCQQSGSWP-HTFGGGTKVEIK 107
                                                                                                  PRT; 107 AA.
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58 IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKV 104

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Humanised anti-alp
Vitronectin alpha-
Kappa light chain
Kappa light chain
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Vitaxin light chai
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557
1 BIVLTQSPATLSLSPGERAT.......CQQSGSWPHTFGGGTKVEIK 107
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Kappa light chain The variable light The variable light Mouse anti-verotox Light chain variab Anti-human TNF-alp Murine CMVS antibo	Ine cays Igg abe Igg abe Igg abe Igg abe an HIV-1 Lence of
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ALIGNMENTS

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Vitaxin, antibody, variable region, heavy chain, light chain, integrin, LM609, inhibitor; integrin-mediated signal transduction; treatment; diagnosis, angiogenesis, restenosis, inflammation, diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.
                                                                                      LM609 grafted antibody light chain variable region protein fragment.
                                                                                                                                                                                                     Location/Qualifiers
                     AAW76006 standard; Protein; 107 AA
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                                                                  (first entry)
                                                                                                                                                                                                     Key
Misc-difference 49
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                                                                                                                                                                                                                                                                                             30-JAN-1998;
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                                          AAW76006;
                                                                                                                                                                                 Mus sp.
           AAW76006
RESULT
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Glaser SM, Huse WD

(IXSY-) IXSYS INC.

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LM609, also related nucleic acid, used to treat, prevent or diagnose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                      This sequence represents a LM609 grafted antibody variable light chain alpediou. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 and can be used to inhibit binding of alphavbeta a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LiM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; anglogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
                                                               integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal
                                               Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitaxin antibody light chain variable region protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                            99.6%; Score 555; DB 19;
100.0%; Pred. No. 3.7e-36;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          macular degeneration; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW76002 standard; Protein; 107 AA
                                                                                                                             Claim 19; Fig 7; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US01826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0791391
                                                                                           angiogenesis or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.6%
Best Local Similarity 100.0
Matches 107; Conservative
WPI; 1998-437472/37.
N-PSDB; AAV49843.
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                                                                                                                                                                                                                                                                                                                                                107 AA;
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                                                                                                                                                                                                                                                                                                                                                 Sequence
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This sequence reperesents the vitaxin antibody variable light chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin—mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis; macular degeneration, cancer, psoriasis, rheumatoid arthritis; macular degeneration, seteoporosis etc.). The antibodies contain non-murine framework regions so are sultable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments in the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grafted antibody; alphaVbeta_3 integrin; angiogenesis; matory; cancer; retina; restenosis; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%; Score 555; DB 19; 99.1%; Pred. No. 3.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitaxin light chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB61360 standard; protein; 107 AA.
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                                         Claim 1; Fig 1b; 129pp; English.
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angiogenesis or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200078815-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                   1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
             diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), discaters associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
 alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis.
                                                                                                                                                                                   Length 107;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                Score 555; DB 22;
Pred. No. 3.7e-36;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain variable region of LM609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB61364 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 7; 132pp; English.
                                                                                                                                                                                Query Match 99.6%;
Best Local Similarity 99.1%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                   Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200078815-A1.
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                                                                                                    osteoporosis
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107 AA;

Sequence

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Gaps
                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                            The sequence shows the humanised mature light chain variable region of the mouse CMV5 antibody. Murine CDRs were used in a human Wol framework to produce a pure humanised immunoglobulin (Ig) which is capable of binding to the gH glycoprotein of cytomegalovirus. The Ig is non immunogenic, due to the human framework, and has a strong affinity for its predetermined annigen. They can be produced in large quantities via recombinant DNA and monoclonal antibody technology. The humanised Igs may be used alone or in combination with chemotherapeutic agents such as see also AAR25721-32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV,
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0
                                                                                                                                                                                                                                                                                   Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus; 9H; light chain; variable region; framework; human; Wol.
 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunoglobulin(s) having murine CDRs in human framework regions - have lower antigenicity; useful for treating e.g. CMV, T-cell disorders, myeloid disorders and auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schneider WP;
                         Indels
                                                                                              99.6%; Score 555; DB 22;
100.0%; Pred. No. 3.7e-36;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                            Humanised VL region of the mouse CMV5 antibody.
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                     AA.
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                                                                                                                                                                                    AAR25729 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                               "mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                               "CDR"
                                                                                                                                                                                                                                                                                                                                                                                                                     "CDR"
                                                                                                                                                                                                                                                                                                                                                                       "CDR"
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                                                                                                                                                                                                                                   (first entry)
                         Conservative
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89..97
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-249842/30
            Similarity
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                                                                                                                                                                                                                                   13-JAN-1993
                                                                                                                                                                                                                                                                                                                        Mus musculus
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                       Matches 107;
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 Query Match
Best Local S
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AAR25729
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97; Conservative
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13-FEB-1989;
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Best Local Si
Matches 97;
                                                                                                                                                                                                             AAB69690;
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections. CMV virus infections demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMY infection.
                                                                                                              Gaps
                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell-
                                                                     ö
                                        Length 107;
                                                                    Indels
                                                                                                                                                                      RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                       Humanised CMV5 antibody light chain SEQ ID NO: 63.
                                        Score 506; DB 13;
Pred. No. 2.2e-32;
                                                                    3; Mismatches
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                                                                                                                                                                                                                                                    AAB69678 standard; Protein; 107
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90US-0590274.
90US-0634278.
                                        90.8%;
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                                                                                                                                                                                                                                                                                                          (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Queen CL, Selick HE;
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                                                       Similarity
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 107
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13-FEB-1989;
28-SEP-1990;
19-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                    97;
                                        Query Match
Best Local 9
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  Sequence
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                                                                                                                                                       19
                                                                    Matches
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Length 107;

Score 506; DB 22; Pred. No. 2.2e-32;

90.8%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections. CMV virus infections demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 2.2e-32;
3; Mismatches 7; Indels
                                                                                                                 Human Wol antibody light chain SEQ ID NO: 87.
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                                                                                                                                                                                                                                                                                                                                 AAB69690 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88US-0290975.
89US-0310252.
90US-0590274.
90US-0634278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AA;
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Humanised antibody; monoclonal antibody; MAb; antibody engineering; mouse; human; vitronectin; alpha v beta 3; receptor; restenosis; cancer; metastasis; rhematoid arthritis; atherosclerosis; anglogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; bl2HZHC-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the light chain variable region (VL) of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody D12H2HC 1-0. It is based on the VL sequence (see AAW84096) of human Kabat subgroup III kappa chain, with complementarity determining regions (CDRs) from the murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84093). 3 Murine framework residues (1, 49 and 60) are retained. The humanised light chain can be expressed in host cells using nucleic acid molecules (see AAV71800) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised D12 VH is also provided (see ANW84097)). The humanised antibodies can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or angiogenic related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and restenosis, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used for
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                                       61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti alpha_v beta_3 vitronectin receptor antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ocation/Qualifiers
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                                                                                                                                                                                                                                       AAW84098 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24..34
/label= CDR1
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/label= CDR2
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/label= CDR3
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Synthetic.
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Region
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Gaps
hyperparathyroidism, Paget's disease, hypercalcemia of malignancy, osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for
                                                                                                                                                                                    1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60

    used for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse; human; vitromectin; alpha-v beta-3; receptor; restenosis; cancer: metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti alpha_v beta_3 vitronectin receptor antibodies - used immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
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                                                                                                                          Length 107;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                               targeted drug therapy, and for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; MAb; antibody
                                                                                                                          Score 504; DB 20;
Pred. No. 3.1e-32;
4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Page 64; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                         AAW84100 standard; Protein; 112 AA.
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                                                                                                                          90.5%;
89.7%;
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-034590/03
                                                                                                                    Query Match
Best Local Similarity
Matches 96; Conserv
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107

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Sequence

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receptor.
The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor.
                                                                                                                                                                                                                                                                                      Kappa; light chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
21 eivltgspatlslspgeratlscrasgsigtnihwyggrpggaprllikyasesisgipa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-EGF receptor antibody 225 esp. of late stage prostatic
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                                                              61 RESGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK
                                                                                                                                                                                                                                                         Kappa light chain variable region of 225RA antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89..97
/label= CDR_3
98..107
/label= framework_4
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/label= framework_3
89..97
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/label= framework_2
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/label= framework_1
24..34
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                                                                                                                                                             AAW08948 standard; Protein; 107
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/label= CDR_2
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95US-0482982
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1996;
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07-JUN-1995;
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                                                                               Gaps
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                                                                                                                             1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotocxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                              Kappa; light chain; reshaped; monoclonal; antibody; 225RA;
human; epidermal growth factor; EGF; receptor; inhibition; growth;
tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric and humanised versions of anti-EGF receptor antibody 225 used for inhibiting tumour growth, esp. of late stage prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RKA. The MAD is specific for the human epidermal growth factor (EGF)
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                                            Length 112;
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                                                                            Indels
                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                           Kappa light chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saldanha JW;
                                              DB 20;
                                                              3.2e-32
                                                                            4; Mismatches
                                              Score 504;
                                                              Pred. No.
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                                            90.5%;
89.7%;
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95US-0482982.
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                                                                            Conservative
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N-PSDB; AAT49345.
                                                           Local Similarity
les 96; Conserv
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112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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07-JUN-1995;
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19-DEC-1996

Giorgio NA,

18-SEP-1997

AAW08946;

61

1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60

inhibitor

Sequence

Query Match

Best Loc Matches

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specific for the human epidermal growth factor (EGF)
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                                                                                                                                                                                                                                                                                                                                                                                     transplantation
                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                           inhibitor.
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                                                                              1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                           Kappa; light chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric and humanised versions of anti-EGF receptor antibody 225 used for inhibiting tumour growth, esp. of late stage prostatic tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RKA. The
                                                 ö
                             Length 107;
                                                7; Indels
                                                                                                           61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                     Kappa light chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saldanha JW;
                            Score 495; DB 18;
Pred. No. 1.5e-31;
                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldstein NI, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                    15..49
||Tabel= framework_2
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|abel= framework_3
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/label= framework_4
                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                                                                                                                     label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Fig 21; 112pp; English.
                                                                                                                                                                              AAW08949 standard; Protein; 107
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/label= CDR_2
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label= CDR_1
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/label= CDR_3
                            88.9%;
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95US-0482982
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                                                                                                                                                                                                                      (first entry)
                                                 94; Conservative
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Best Local Similarity
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107
                                                                                                                                                                                                                                                                                                              Homo sapiens
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07-JUN-1995;
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The present sequence represents the variable light chain of humanised antibody L3.17. The antibody is effective in modulating humoral immune response against r cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases,
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                               1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                     The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain variable region; chimeric antibody; anti-CD40 antibody; chi220; humoral immune response; T cell dependent antigen; collagen induced arthritis; transplant induced rejection; T cell mediated disorder; autoimmune disease; inflammatory disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody that binds human CD40, for treating T cell mediated
                                                                                                                                                               Length 107;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The variable light chain of humanised antibody L3.17.
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                                                                                                                                                           Score 495; DB 18;
Pred. No. 1.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watkins JD,
                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Page 33-34; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAY30205 standard; Protein; 107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                         88.9%;
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Best Local Similarity 87.9'
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Best Local Similarity 88.8
Matches 95; Conservative
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                                                                                             Gaps
                                                                                                                  EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                Light chain variable region; chimeric antibody; anti-CD40 antibody; chil220; humoral immune response; T cell dependent antigen; collagen induced arthritis; transplant induced rejection; T cell mediated disorder; autoimmune disease; inflammatory disease;
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                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that binds human CD40, for treating T cell mediated
                                                                                          Indels
                                                                                                                                                                    The variable light chain of humanised antibody F4.
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Thorne BA, Watkins JD, Wu
                                                               Score 490; DB 20;
Pred. No. 3.7e-31;
5; Mismatches 7;
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                                                               Query Match
Best Local Similarity 88.8%;
Matches 95; Conservative
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Huse WD, Siadak AW,
  and transplantation
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                           107 AA;
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disorders
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DB 20;

87.8%; Score 489;

Query Match

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                Gaps
                                            9
                                                                        1 elvltgspatlslspgeratlscrasgsisdylhwygqkpgqaprlliyyashsisgipa 60
                                                                                                                                                                                                                                                                                                                                         human;
                                           EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA
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                                                                                                                                                                                                                                                                                                                        Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1; monoclonal antibody; light chain; mouse; humanised antibody; hu Escherichia coll; VTEC; infection; haemolytic uraemic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region 2"
                                                                                                                                                                                                                                                                                                Mouse anti-verotoxin II antibody VTml-1 humanised VL region
               Indels
                                                                                                                   61 rfsgsgsgtdftlillillisslepedfavyycqhghsfpwtfgggtkveik 107
                                                                                                     61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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Pred. No. 4.4e-31;
5; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanized antibody binding to verotoxin II
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...te= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                        AAY32407 standard; Protein; 127
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                                                                                                                                                                                                                                                                    (first entry)
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109..117
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                                                                                                                                                                                                                                                                                                                                                                        HUS; therapy.
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position of the MuVTml-1 antibody heavy or light chain variable region framework. Such humanized antibodies have an affinity for VT2 that is 3., 5 or 10-times that of MuVTml-1. They are used for treating a patient suffering from, or at risk of, the toxic effects from VT2 (claimed), especially for treating verotoxin producing Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).
                                                                                                                                                                                              Sequence 127 AA;
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.; 0 Gaps ö 86.9%; Score 484; DB 21; Length 127; 88.8%; Pred. No. 1.2e-30; Live 5; Mismatches 7; Indels (Query Match 86.9% Best Local Similarity 88.8% Matches 95; Conservative

1 BIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60

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Search completed: October 11, 2001, 12:01:58 Job time: 968 sec

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Sequence 12, Appl Sequence 12, Appl Sequence 8, Appli Sequence 8, Appli Sequence 13, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl

Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli Sequence 25, Appli

Sequence 27, Appl Sequence 27, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli

Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

Sequence 25,

Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl

Sequence 10,

Sequence 114, App Sequence 12, Appl

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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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Recombinant Human
Acids Encoding Same and Methods of Use
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STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
               US-08-485-246-6
PCT-US99-21646-27
US-09-397-569-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-127-721-6
US-08-476-176-6
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US-08-485-246-8
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TITLE OF INVENTION: Anti-Alpha V Beta 3
TITLE OF INVENTION: Antibodies, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08790540 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEFHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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                                                                                                                                                                                                                                                                                                            1 EIVLTOSPATLSLSPGERAT.......COOSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                  Search time 239.24 Seconds
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1: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*

9: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*

10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

12: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-791-391-4
US-08-791-391-4
US-08-791-391-8
US-08-791-391A-4
US-08-791-391A-4
US-09-1016-061-4
US-09-339-922A-4
US-09-339-922A-3
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                                                                                                                                                                October 11, 2001, 12:06:42
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Score

1084597861

Result

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Sequence 4, Application US/08791391
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
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TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
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GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Nucleic Acids Encoding Same and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
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Pred. No. 5.5e-49;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 535-9001
TELEFRAX: (619) 535-8001
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States
ZIP: 92122.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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IBM PC compatible
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Best Local Similarity 99.1%;
Matches 106; Conservative
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: United States
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell 6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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STATE: Californi
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GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF CORPESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 0S/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                 99.6%; Score 555; DB 11; 100.0%; Pred. No. 5.5e-49;
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                                                                                                                                                                                                                               Best Local Similarity 100.0%; Pred. No. 5.5 Matches 107; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIGSRATION NUMBER: 31,815
REFERENCE/CDCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
                                                TOPOLOGY: Ilnear
MOLECULE TYPE: protein
US-08-790-540-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4370 La CITY: San Diego STATE: California COUNTRY: United SIP: 92122
                              amino acid
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RESULT 6
US-08-791-391A-32
Sequence 32, Application US/08791391A
Sequence 32, Application US/08791391A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF SEQUENCES: 32
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                           1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                      1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIKYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLEPEDFAVYCQQSGSWPHTFGGGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.6%; Score 555; DB 11; Best Local Similarity 100.0%; Pred. No. 5.5e-49; Matches 107; Conservative 0; Mismatches 0;
                                                                   Score 555; DB 11;
Pred. No. 5.5e-49;
                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIGSTRATION NUMBER: 31,815
REFRENCE/CDCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09016061
                                                                   99.68;
99.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 107 amino acids TYPE: amino acid
                                                                Query Match
Best Local Similarity 99.18
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4370 La Joi
CITY: San Diego
STATE: Callifornia
COUNTRY: United Sta
ZIP: 92122
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  US-08-791-391A-4
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US-09-016-061-4
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GENERAL INFORMATION:
APPLICANT: HUSE, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 32
CORRESPONDED ADDRESS:
CORRESPONDE Campbells Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 555; DB 11;
Pred. No. 5.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.6%; Scc.
100.0%; Pre
0;
                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9091
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                      : 107 amino acids
amino acid
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amino acid
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: United States
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Best Local Similarity 100.
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy (
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                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Sequence 4, Application US/09339922A

Sequence 4, Application US/09339922A

GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
TITLE OF INVENTION: Acids Encoding Same and Methods of Use
TITLE OF INVENTION: Acids Encoding Same and Methods of Use
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT APPLICATION 1005: 112

NUMBER OF SEQ. DE NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: grafted ; OTHER INFORMATION: antibody variable region US-09-339-922A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%; Score 555; DB 17; Length 107; Best Local Similarity 99.1%; Pred. No. 5.5e-49; Matches 106; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLEPEDFAVXYCQOSGSWPHTFGGGTKVEIK 107
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                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CALLCATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.6%; Score 555; DB 14; Best Local Similarity 100.0%; Pred. No. 5.5e-49; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELLING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: PIX 2965
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 107 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-09-016-061-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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SEQ ID NO 4
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GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
COMMESSPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                  APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Anti-bodies, Nucleic Acids Encoding Same and Methods of Use
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CADPUTE: P.112.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1998
CLASSIFICATION NUMBER: US 08/791,391
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: PIX 2965
TELECOMMULICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9049
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 99.19
Matches 106; Conservative
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                                                                                                                         NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                                                                        STREET: 4370 La
CITY: San Diego
STATE: Californi
GENERAL INFORMATION:
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APPLICANT: Johak, Zdenka L.
APPLICANT: Johanson, Kyung O.
APPLICANT: Taylor, Alexander H.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 506; DB 17
Pred. No. 6e-44;
                                                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                             FILING DATE: 28-SEP-1990
PROOR APPLICATION DATE:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PROOR APPLICATION DATE:
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M:
REGISTRATION NUMBER: 30,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/US98/04987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application PC/TUS9804987
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIF: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12 March 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.8%;
90.7%;
13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.7%
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-325-000-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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PCT-US98-04987-10
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                                                                                            APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
APPLICANT: Hu, Herren
TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
TITLE OF INVENTION: Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT APPLICATION NUMBER: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 555; DB 17;
100.0%; Pred. No. 5.5e-49;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
STATE: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa - Arg or Met
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: antibody variable region
US-09-339-922A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 07/310,252
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             , Application US/09339922A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09325000 GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Co, Man Sung
APPLICANT: Schneider, William P.
APPLICANT: LandOllí, Nicholas F.
APPLICANT: Coelingh, Kathleen L.
APPLICANT: Selick, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.C
Matches 107; Conservative
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                           Sequence 32, Applica
GENERAL INFORMATION
APPLICANT: Huse, N
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
                                 US-09-339-922A-32
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                                                                                                                                                                                                                                                                                                                  SEQ ID NO 32
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Gaps
                                          1 EIVLTQSPATLSLSPGERATLSCQASQSISNHLHWYQQRPGQAPRLLIXYRSQSISGIPA 60
                                                               1 DIVLTQSPGTLSLSPGERATLSCRASQSISNHLHWYQQKPGQAPRLLIKYASQSISGIPS 60
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  7; Indels
                                                                                                                                               61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNSWPFTFGQGTKVEIK 107
                                                                                                                          61 RESGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                              APPLICANT: SmithKilline Beecham Corporation
APPLICANT: Jonak, Zdenka L.
APPLICANT: Jonak, Zdenka L.
APPLICANT: Johnson, Kyung O.
APPLICANT: Johnson, Kyung O.
APPLICANT: Taylor, Alexander H.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
NUMBER OF SEQUENCES: 45
CORRESPONDENES: ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQSGSWPHTFGGGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/04987
    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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REFERENCE/DOCKET NUMBER: P50629-1
                                                                                                                                                                                                                                                                 Sequence 14, Application PC/TUS9804987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/039,609
FILING DATE: 12 MArch 1997
ATTONNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09380910; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 amino acids amino acids
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein PCT-US98-04987-14
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ZIP: 19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                PCT-US98-04987-14
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US-09-380-910-14
  96;
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    Matches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,910
FILING DATE: 24-Apr-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jonak, Zdenka L.
Johanson, Kyung O.
Taylor, Alexander H.
INVENTION: Humanized Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmittKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                            Score 504; DB 1; I
Pred. No. 9.7e-44;
4; Mismatches 7;
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Pred. No. 9.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/039,609
FILING DATE: 12 March 1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09380910 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                            Query Match 90.5%;
Best Local Similarity 89.7%;
Matches 96; Conservative
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89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                   LENGTH: 107 amino acids
                               TELEFAX: 0.10-270-4026
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           MOLECULE TYPE: protein PCT-US98-04987-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                        amino acid
                                                                                                                                           TOPOLOGY: linear
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Best Local Similarity
                       TELEPHONE:
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Johanson, Kyung O.
Taylor, Alexander H.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
APPLICANT: SmithKline Beecham Corporation Jonak, Zdenka L.
                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P50629
TELECHANNICATION INFORMATION:
TELEFRAX: 610-270-5015
TELEFRAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-380-910-14
                                                                                                                                                                                                                                                                                                                                                                                                NAME: King, William T.
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ö Gaps ; 0 90.5%; Score 504; DB 17; Length 112; 89.7%; Pred. No. 1e-43; Live 4; Mismatches 7; Indels Query Match
Best Local Similarity 89.73
Matches 96; Conservative

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